

## STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 108672

TO: Manjunath N Rao

Location: CM1/10D01/10A11

Art Unit: 1652

Tuesday, November 25, 2003 Case Serial Number: 10/005306 From: Paul Schulwitz

Location: Biotech-Chem Library

CM1-6B06

Phone: 305-1954

paul.schulwitz@uspto.gov

### Search Notes

Examiner Rao,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz Technical Information Specialist STIC Biotech/Chem Library (703)305-1954



### STIC-Biotech/ChemLib

108670

From:

Chan, Christina

Sent: To: Subject: Wednesday, November 19, 2003 3:32 PM Rao, Manjunath N.; STIC-Biotech/ChemLib

RE: RUSH sequence search request for 10/005,306

### Please rush. Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message----

From: Sent: Rao, Manjunath N. Wednesday, November 19, 2003 2:48 PM

To: Chan, Christina

Subject:

RUSH sequence search request for 10/005,306

Hello Christina,

Please authorize the request below as RUSH. The reason being this is an IFW due this bi-week.

From:

Manjunath N. Rao

Art Unit 1652, Room 10A11 Mail Box in Room 10D 01

Phone: 306-5681

Phone: 306-56

Date:

11-19-03

Please search the following as soon as possible for application with serial number 10/005306

SEQ ID NO: 9 against all <u>commercial amino acid databases</u>, <u>issued patents/published</u>
 <u>applications database</u> and <u>pending application database</u>. Please provide a <u>print</u> of
 all <u>results</u>.

If you have any questions please call me at the above phone number.

Other:

Searcher:
Phone:
Location:
Date Picked Up: 11/2:
Date Completed: 1/725
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:

NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:

VENDOR/COST (where applic.)
5TN:
DIALOG:
Questel/Orbit:
DRLInk:
Lexis/Nevis:
Sequence Sys.:
WWW/Internet:
Other (specify):

### T<del>ira</del>nks

Manjunath N. Rao, Ph.D. Biotechnology Patent Examiner Art Unit 1652, Room 10A11 Mail Box in 10D01 Crystal Mall 1, USPTO.

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

## TYPE OF SEARCH: NA Sequences: AA Sequences: Structures: Bibliographic: Litigation: Full text: Patent Family: Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
www/Internet:
Other (specify):

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compagen Ltd.	
OM protein - protein search, using sw model	
Run on: November 21, 2003, 13:44:10 ; Search time 41 Seconds (without alignment) 100 100 100 100 100 100 100 100 100 10	
Title: US-10-005-306-9 Fittle: 1167 Sequence: 1 LitarriorFGFIONSNATLSDQLAQAISDHYPVFVMLK 260 Sequence: 1 LitarriorFGFIONSNAT	
Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5	
Searched: 1107863 segs, 158726573 residues	
Total number of hits satisfying chosen parameters: 1107863	
Minimum DB seq length: 0 Maximum DB seq length: 2000000000	
Post-processing: Minimum Match Ot Maximum Match 1004 Liscriff first 45 summaries	
A. General, JAN1013;   A. General, JAN1019;   A. GENERAL, General, General, JAN1019;   D. G.	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.	

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	140W4R0C80

## ALIGNMENTS

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asthma; bubeculosis.
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/note= "wild-type Asn is replaced by Lys"
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Misc-difference 74
                   AAW49937 standard; protein; 260 AA.
                                                                         Human mature DNase I variant N74K.
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Synthetic.
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                                                              /label= N74R
/note= "wild-type Asn is replaced by Arg"
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Location/Qualifiers
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RESULT 3

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05-JUN-1998

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99.6%; Score 1362; DB 19; Length 260;
Best Local Similarity 99.6%; Pred. No. 1.2e.166

Matches 259; Conservative 0; Mismarches 1; Indels 0;
Matches 259; Conservative 0; Mismarches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present eacquores is that of human mature Mohase I Activ-resistant variants of human Misse I test advantages of page of the control bronchitis. They diseases or ignorates by cysic fibrosis or chronic bronchitis. They can be used for reducing the viscollasticity or viscous consistency of DNA-contg. material in a patient. They can be used for tracting e.g. acute or chronic bronchial pulmonary disease, asthma. systemic lauva crystamanceses. They can be used for tracting assign of acute or chronic bronchial pulmonary disease, asthma. systemic lauva derychamacoses. They can be used for tracting assign with an active resistant may be used on the patient is an appropriate condidate for broad decoming whether the patient is an appropriate condidate for broad mental conditions of actin the brease of actin mass of acting the very select into the presence of actin as compared to native human microlytic activity in the presence of actin as compared to native human microlytic activity in the presence of actin as compared to native human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKIAAFNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNINQDAP 60
                                                                                                                                                                        human mature DNase I, actin-resistant variant; treat; pulmonary disease; disorder; cystic fibrosis; htmonic bronchitis; viscoelasticity; viscoussiculity; viscousistency; actima; systemic lupus erythematosus; in vitro; assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New actin-resistant human DNasel variants - used for reducing the "viscous combistency of DNA-confor material, e.g. for treating chronic bronchitis or cystic fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1362; DB 17; Length 260;
Pred. No. 1.2e-146;
0; Mismatches 1; Indels 0;
             AAW03666 standard; protein; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 LSDQLAQAISDHYPVEVMLK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ulmer JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Fig 1; 149pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.6%;
Matches 259; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                         96WO-US02421.
                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0540527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-US02366
                                                                                          02-MAY-1997 (first entry)
                                                                                                                                      Wild type human DNase I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shak S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-402370/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 AA;
                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                        WO9626279-A1.
                                                                                                                                                                                                                                                                                                                                                                                         21-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                    10-0CT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                    29-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lazarus RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                     AAW03666,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNase I.
          셤
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This sequence represents the human mature DNase 1. This sequence can be embestured and sequence for the control of the control
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DIYHYVVSEPLGRNSYKERYLEVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 RFTEVREFAIVPLHAAFGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 RFTEVREFALVPKHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WSSIRLWISPIRGWLIPDSADTIATPTHCAYDRIVVAGMLLRGAVVPDSALPPNFQAAYG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 WSSIRLMISPIRGWLIPDSADTTATPTHCAYDRIVVAGWLLRGAVVPDSALPFOAAYG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LKIAAFNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, DNase I, respiratory; mucolytic; antiasthmatic; dermatological; imminosuppressant, antifiliamanchy; actin-tessistant; variant; obtenic dotronic bronchite; pneumonia; bronchitectssis, empkysema; asthma; systemic lupus erythematosus; DNA hydrolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
   Hyperactive variant of human DNasel - useful to treat pulmonary disease, e.g. cystic fibrosis and systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.6%; Score 1362; DB 19;
99.6%; Pred. No. 1.2e-146;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM51552 standard; protein; 260 AA.
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                                                                         Disclosure; Fig 1; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 LSDQLAQAISDHYPVEVMLK 260
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Best Local Similarity 99.6*
Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2001041360-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                     DIYHYVVSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120
                                                                                                                                                             RFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPSQ 180
Mature DNase I; variant; hyperactive; pulmonary disease; pneumonia; systemaind: Unpus erychhematosus; cystic fibrosis; bronchitis; emphysema; asthma; tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 14
/note= "Thr at this position can be substituted to create a variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Gln at this position can be substituted
to create a variant"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 13 /note= "Glu at this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "His at this
to create a
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/note= "Ser at this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW49929 standard; protein; 260 AA
                                                                                                                                                                                                                                                                                                                                                LSDQLAQAISDHYPVEVMLK 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
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DIYHYVVSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LKIAARNIQIFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 LKIAARNIQTFGETKKSNATLVSXIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFTEVREFALVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDPNAGCSYVRPSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Two components of a recombinant prepr. of DNase are identified and characterised. A separation method and uses of these components are given in the specification:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Purified forms of non-deamidated and deamidated human DNase - for treatment of pulmonary distress, vygito fibrosis, chronic bromchitis, emplysema, pneumonia, asthma, tuberculosis and fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.6%; Score 1362; DB 15; 99.6%; Pred. No. 1.3e-146; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                           23..282
/label= mat_protein
                                                                                                1..22
/label= sig_peptide
                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shire SJ, Sliwkowski MB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAM52142 standard; Protein; 282 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 1, 38pp; English
                                                                                                                                                                                                                                                                                                                         93WO-US05136
                                                                                                                                                                                                                                                                                                                                                                       92US-0895300
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Best Local Similarity 99.6
Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQS4429
                                                                                                                                                                                                                        W09325670-A1.
                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                         28-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                       08-JUN-1992;
                                                                                                                                                                                                                                                                       23-DEC-1993,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Frenz J,
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                                                                                            Peptide
                                                                                                                                               Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention rathese to the name Dase I sactio-resistant variants and the multic acids that enrode them the extract are used for the treatment of cystic fibrosis and chromat broath are used for the broom-hieratsis employeem, asthem, and systemic lupus presentions uses in Mase I reduces the viscolaristicity of following vectorismscous in such diseases as premucial and cystic fibrosis, therefore siding in the clearing of respiratory armays. The presence of actin, thus in DNA-Hydrolytic activity of DNSes I is inhibited. Actin.resistent DNSes I was increased encolytic activity and in some cases have increased encolytic activity and in some cases have increased encolytic activity as operate session setting the minibited. The present sequence is native human DNSes I seems have human DNSes I seems have human DNSes I seems have human DNSes I seems and the present sequence is native human DNSes I seems have human DNSes I was a second of the season of the present sequence is native human DNSes I was a second of the page of the present sequence is native human DNSes I was a second of the present sequence is native human DNSes I was a second or season when the present sequence is native human DNSes I was a present sequence is native human DNSes I was a present sequence is native human DNSes I was a present sequence is native human DNSes I was a present sequence is native human DNSes I was a present sequence is native human DNSes I was a present sequence in the present sequence in the present sequence is native human DNSes I was a present sequence of the present sequence of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
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                                                                                                                                                                                                                                                                                                                                    Actin-resistant variants of human DNase I and encoding nucleic acids, useful for treating cystic fibrosis and chronic bronchitis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 99.6%; Score 1362; DB 23; Length 260; BEEL Local Similarity 99.6%; Pred. No. 1.22-4.6 Median of Matches 259; Conservative 0; Marahachas 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNace; non-desmidated; deamidated; pulmonary distress; oystic fibrosis; chronic bronchitis; emphysema; pneumonia; schima; tuberulosis; fungal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR45356 standard; Protein; 282 AA
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                                                                                                                                                                                                                                    Ulmer JS:
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Fig 1; 25pp; English.
                                                          95US-0540527.
97US-0929995.
95WO-US02366.
96US-0403873.
               2001US-0796774.
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(first entry)
                                                                                                                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                    Lazarus RA, Shak S,
                                                                                                                                                                                                                                                                                      WPI; 2002-017217/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 AA;
                                                                                                        24-FEB-1995;
24-MAR-1996;
               28-FEB-2001;
                                                             0-0CT-1995;
                                                                                     15-SEP-1997;
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RFIEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGGSYVRPSQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised monoclonal antibody; polymorphic epithelial mucin, PEM1; cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LKIAAFNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 LKIAAFNIQIFGEFKWSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIYHYVVSEPLGRKSYKERYLFVYRPDQVSAVDSYXYDDGCEPCGNDTFNREPAIVRFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 RFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPSQ
                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a process for preparing recombinant decoyribonoutease I (Dakes.) You (Dakes.) You be decoyribonoutease I used to treat diseases in the respiratory system. The present esequence represents a Dakase-I which is given in the exemplification hip present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 282;
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                                                                                                                                                                                                                                                                                                                                                 Process for preparing recombinant deoxyribonuclease
                                                                                                                                                                                                                                                                                                                                                                                   Example 1, Page 18-19 (Disclosure); 23pp, Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.6%; Score 1362; DB 24;
99.6%; Pred. No. 1.3e-146;
ive 0; Mismatches 1;
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                                                                                                                                                                                                                     (HUAD-) HUADA GENE RES CENT BELJING.
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                                                                                                                                               19-JAN-2001; 2001CN-0101653
                                                                                                                                                                                 19-JAN-2001; 2001CN-0101653
     respiratory system disease.
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Matches 259; Conservative
                                                                                                                                                                                                                                                          Wang C;
                                                                                                                                                                                                                                                                                         WPI; 2003-240395/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 AA;
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                                                                                                                                                                                                                                                          Feng X,
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                                       Unidentified.
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                                                                                                                                                                                                                                                       Liu S,
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Humanised monoclonal antibody; polymoxphic epithelial mucin; PEM1,
cytotoxic; endonuclease; DNase 1; human; cytostatic; cancer; apoptosis.
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                                                                                                                                                                                                                                                                                                                                                          OMOVel, compound used to treate cancer has tracter ceal-reportific portion conversity in tunnised monoclonal antibody having specificity for projumorphic optibulal mucin, and cytotoxic portion having applying editivity -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.6%; Score 1362; DB 22;
ilarity 99.6%; Pred. No. 1.3e-146;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deoxyribonuclease I protein SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Figure 1, 176pp, English.
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                                                                                                                                                                                               03-APR-2000; 2000GB-0008049.
                                                                                                                                                             26-MAR-2001, 2001WO-GB01324
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                                                                                                                                                                                                                                                  (ANTI-) ANTISOMA RES LTD
                                                                                                                                                                                                                                                                                                                        WPI; 2001-662969/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                       WO200174905-A1.
                                                        Homo sapiens
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                                                                                                                           11-OCT-2001.
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                                                                                                                                                                                                                                                                                      Young RJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 LKIAAFNIQTFGETKASNATLUSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAP 317
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99.6%; Score 1362; DB 22;
Best Local Similarity 99.6%; Pred. No. 3.2e-146;
Best Local S29; Conservative 0; Mismatches 1;
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                                   26-MAR-2001; 2001WO-GB01324
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11-OCT-2001
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                                      26-MAR-2001; 2001WO-GB01324.
                                                                                03-APR-2000; 2000GB-0008049
                                                                                                      02-OCT-2000; 2000US-237159P.
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Matches
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The invention relates to a compound with comprises a target cell-especific portion, comprising an humanised monoclonal antibody having specificity for polymorphic epithelial mucin (RBW) or its antigen having fragmen and a cytocock portion having endomucleolytic ectivity, exemplified by AMMAZI44-AAMAZI68 and encoded with AAMAZI44-AAMAZI68 and encoded the AAMAZI44-AAMAZI68 and encoded the AAMAZIA4-AAMAZI68 and encoded and accompound has cytostatic activity useful for treating cancer and accing as a potential inducer of apoptosis.
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cytotoxic, endonuclease, DNase I, human, cytostatic, cancer, apoptosis.
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99.6%; Pred. No. 3.2e-146;
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cytotoxic; endomuclease; DNase 1; human; cytostatic; cancer; apoptosis.
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Pred. No. 3.2e-146;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20, Figure 15; 176pp; English.
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Best Local Similarity 99.6%;
Matches 259; Conservative
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                                                                                       26-MAR-2001, 2001WO-GB01324
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02-OCT-2000;
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2000GB-0008049

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Novel compound used to treat cancer has tratege cell-specific portion operating humanised monoclonal antibody having specificity for perjormorphic optibilish mucin, and optotoxic portion having endomucleolytic activity -
                                                                                                                                                                                                                                                            Claim 20; Figure 6; 176pp; English
                                                   26-MAR-2001; 2001WO-GB01324
                                                                                        02-OCT-2000; 2000US-237159P.
                                                                                                                (ANTI-) ANTISOMA RES LTD
                                                                                                                                                                  WPI; 2001-662969/76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a compound which comprises a target antibody, cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (PBM) or its antigen having frequent and a vyctocoxic portion having endomuclosolystic activity, binding frequent and a vyctocoxic portion having endomuclosolystic antivity, exemplified by AAMSISH4-AAMSISH and encoded by ABMAZESTARADSH THE compound has vycotatic activity useful for treating cancer and activity a poptosis.
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Chimeric - Rhesus macaque polyoma virus.
                                                                                                                                                                                                                                                Claim 20; Figure 17; 176pp; English
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                                         26-MAR-2001; 2001WO-GB01324
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                11-OCT-2001.
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The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial macin (EBM) or its antigen hindrag fragment and a verocoxic portion having endoundled/ptic exemplified by AbMS2184-AbMS2188 and encoded specification polymorphic compound has cytostatic activity useful for treating cancer and acting as a potential inducer of approprise.
                                                                                                                                                                                                                                                                                                                                                                                                                                              DIYHYVVSEPLGRKSYKERYLPVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPALVRFFS 120
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Best Local 8
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# GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

November 21, 2003, 13:46:05 ; Search time 21 Seconds Run con:

(without alignments) 1190.660 Million cell updates/sec

1 LKIAAFNIQTFGETKMSNAT.....LSDQLAQAISDHYPVEVMLK 260 US-10-005-306-9 Perfect score: Seguence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

Total number of hits satisfying chosen parameters: 283308 segs, 96168682 residues

Searched:

Minimum DB sed length: 0 Maximum DB sed length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:\* Database :

pirl: pir2: pir3:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Query

No	Score	Match	Match Length	DB	di	Description
-	1362	99.6	282	-	NDH01	deoxyribonuclease
8	1129	82.6	284	н	S13676	deoxyribonuclease
~	1127	82.4	284	7	JC2526	deoxyribonuclease
4	1072	78.4	262	~	A26324	deoxyribonuclease
ß	1067	78.1	282	-	NDBOA	deoxyribonuclease
w	1061	77.6	260	Н	B26325	deoxyribonuclease
7	591	43.2	305	~	JC5361	deoxyribonuclease
80	464.5	34.0	302	N	JC4633	DNase I-like endon
6	128	9.4	1067	~	D75625	probable extracell
10	100.5	7.4	1646	н	WMTMS2	186K protein - cuc
11	94	6.9	1070	~	T31332	nuclease - Aeromon
12	93.5	6.9	2163	7	\$50675	pre-mRNA splicing
13	91	6.7	488	~	T41160	hypothetical prote
14	91	6.3	761	N	AB1848	hypothetical prote
15	90	9.9	337	N	G82453	lipase, GDXG famil
16	88.5	6.5	534	ď	AB0392	probable carbohydr
17	88	6.4	929	~	T17392	vrli protein - Dic
18	87	6.4	441	~	H96817	hypothetical prote
19	87	6.4	779	~	E83157	hypothetical prote
20	87	6.4	831	N	T05265	coat protein gamma
21	86.5	6.3	299	N	H82845	2,3,4,5-tetrahydro
22	85.5	6.3	916	~	JT0396	reverse transcript
23	85.5	6.3	991	~	A99334	hypothetical prote
24	84	6.1	267	~	\$38044	hypothetical prote
52	84	6.1	394	N	F90598	
26	83.5	6.1	345	N	T48351	adenosine kinase-1
27	83.5	6.1	1102	N	T02782	probable relaxase
28.	83	6.1	742	~	C83061	probable TonB-depe
29	87	0.9	403	N	T17501	major capsid-like

L2 protein - human	membrane nuclease	annexin IV - pig	probable D-lactate	genome polyprotein	annexin IV - bovin	phosphoglycerate t	acid phosphatase (	subtilisin-like pr	aerobactin biosynt	protein T24B12,10	hypotherical prote	exodeoxyribonuclea	hypothetical prote	two-component hybr	conserved hypothet
P2WL39	C82885	LUPG4	H72744	GNNY1B	LUBO4	882426	S53476	S61986	T44481	G88109	H90481	G71673	T48367	AH2090	AD0890
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6.0	6.0	6.5	5.9	5.9	6.6	5,9	5.9	5.8	5.8	5.8	5.8	8.8	9.9	8.8	5.7
82	81.5	81	80.5	80.5	80	80	80	79.5	79.5	79.5	79.5	79	79	79	78.5
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A, Accession: A38417

Alexicanie Frychognie RRN, A. Residues 1.-282 c881N. RN, Cares-references: GR: 1.-282 c881N. RN, Cares-references: GR: 1.-282 c881N. RN. Cares-references: GR: 1.-282 c881N. RN. Cares-references: GR: 1.-282 c881N. J.; Rinkade, P. R.; Kaurer-Fogy, 1.; Kahn, J.; Batton, R.W. R. Roeenstreich, D. L.; Thu, J. H.; Kinkade, P. R.; Kaurer-Fogy, 1.; Kahn, J.; Batton, R.W. A.; Tritle: A human urind-earlyed interleukin 1 inhibitor. Romology with deoxyribonucless A.; A. Reference number: PLO036; WIID:8903596; RKID:3283467

Albeleanle Viger protezin Albesdader 23-25, Xr. 27-20, Xr. 32-39, Xr. 41-43, Xr. 45, 73-59 «ROS» Albesdader 23-25, Xr. 54, 840, W.; lidds, R.; Tanakk, Y.; Kishl, K. J. Bicchem. 109, 393-399, 199 Albesdader and spenetically polymorpho decoyyzhomolesse; purification, characterizati Albesderence number: Rodist4; MUID-91115795; WHID:2277032

A; Molecule type: protein A; Residues: 23-39,'X',41-49 <YAS> A, Accession: PS0144

A.Gome of GRIPANSEI, DASSI, JA2445, OKIN.125505
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Query Match 99.6%; Score 1362; DB 1; Length 282; Best Local Similarity 99.6%; Pred. No. 1.1e-17; Indels Matches 299; Conservative 9; Mismatches 1; Indels

9 1 LKIAAPNIQTPGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAP 0; Gaps ŝ

23 LKIAAFRIQIFFGETKMSNATLVSYIVQILSRYDIALVQBVRDSHLYAVGKLLDNLNQDAP 82

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121 RFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPSØ 180

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A.Reference number: JC6532; NUID:98137790; PMID:946931	Matches 202; Conservative 28; Mismatches 29; Indels 0; Gaps 0,
A;Accession: 0.0534 A;Molecuse: 1.7ps: MRNA A:Residence: 1.282 //HF.	9
A.Cross.references: GB:AJ001538; NID:92546887; PIDN:CAA04819.1; PID:92546888 R.Liao, T.H.; Salnikow, J.; Moore, S.; Stein, W.H.	Db 23 LKIAAFWIRTFGETKWSWATLASYIVRIVRRYDIVLIQEWRDSHLWAWGKLLGYLWQDDP 82
J. Biol. Chem. 248, 1489-1495, 1973  Trille Bowline pancestic deoxyritolouclease A. Isolation of cyanogen bromide peptides: A. Reference number. 2007-31.	OY 61 DTYHVVUSEPLORKSYKERYLEVYREDOVSAVDSYYYDDCCEPCANDFRIEBALVRFFS 120
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A, Nocalduces - 23-49, 53-59, 'ED', 62-248, 'GP', 251-282 <lii> A, Experimental source: deoxyribonuclease A</lii>	QY 121 RFTEYRERALVPLHAAPGOMAKEIDAL/XDYYLDVQBKWGLEDVMLMGDFNAGCSYVRPSQ 180 Li-li
A;Note: this sequence revised in reference A38938 A;Note: disulfide bonds link residues 123-126 and 195-231, the former bond can be reduce	
Kilado, T.H.; Salnikow, U.; Mooke, S.; Stein, W.H. J. Biol. Chem. 267, 1997, 1997 A.Reference number. A.Ref948, MITH. 022)1846. DMTD. 1148610	203 WSSIRERESSFROWLIPDSADTFATSTNCAYDRIVVAGSLLOSSVVPGSAAPFDFQAAYG
A;Contents: annotation; revisions R;Salnikow, J.; Murphy, D.	Qy 241 LSDQLAQAISDHYPVEVML 259
J. Biol. Chem. 248, 1499-1501, 1973. A.Title: Bowine pancreatic decoyithonucleases A and C. A proline for histidine substitut A/Reference number: A/2124; WIDD:7314929; PMID:4734177	Db 263 LSNEWALALSDHYPVEVTL 281
A, Accession: A32, Protein A, Modecule type: protein A, Residues: 23-49,53-59, EQ', 62-142, P', 144-248, GP', 251-282 «SAL»	RESULT 6 B2635 Geoxyribonuclease I (EC 3.1.21.1) - sheep
r, paperimentan boutce; ucoxy, include tease C. Rillao, T.H. Rillao, T.H. J. Biol. Chem. 249, 2354-2356, 1974	C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
A,Title: Bovine pancreatic deoxyzibonuclese D. A,Reference number: A92148; MUID:74143471; PMID:4856650	C,Avcession; 5265.25 F,Paudel, H.K.; J, Jao, T.H. J, Blol, Chem. 261, 1601-16017, 1984
A;Accession: A92148 A;Molecule type: protein	A)Title: Comparison of the three primary structures of deoxyribonuclease isolated from
A:Residues: 23-49,53-59,'EQ',62-142,'P',144-248,'GP',251-282 <li2> A:Reperimental source: deorgy:thorniclesse D</li2>	G. 100-17 publicated mainto dalla seguenica OL DOVINE DARSe. A;Reference number: A26325; MUID:87057261; PMID:3782105 A;Accession: B26325
Association of Association was a street from the A and B forms in having 143-Pro; the only difference bound to Association with the only difference of the control of the c	A;Molecule type: protein A;Residues: 1.260 <pau></pau>
Kirandei, Lik., ilao, T.H. - Estol. Chem. 261, 16012-16017, 1986 Armitle: Commarian of the three orders	C;Superfamily: deoxyribonuclease I
eviously published amino acid sequence of bovine DNase, A.Reference number. 126325. MITD. 2005361. Wath. 200310	Query Match 77.6%; Score 1061; DB 1; Length 260;
A;Accession: A26325 A;Accession: A26325 A;Molecule type: protein	Best Local Similarity 77.2%; Pred. No. 4.9e-90; Matches 200; Conservative 32; Mismatches 27; Indels 0; Gaps 0;
A.Residues: 39, /x', 41-58 <pau> R.Price, P.A.: Moore, S.: Stein, W.H.</pau>	OY 1 LKIAAFNIQTFOETKWSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAP 60
J. Biol. Chem. 244, 924-928, 1969 AyTitle: Alkylation of a histidine residue at the active site of howing manywestin Annual	Db 1 LKIAAFNIRTFGETRAKSNIVRILRRYDIALIEQVRDSHLVAVGKLLDDLNQDDP 60
A;Reference number: A92054; MUID:69184134; PMID:4976790	
A;Note: in the presence of divalent cations, His-156 is alkylated by iodoacetate with controlli, T.E.; Stein, W.H.	DD 61 NSYHYVVSEPLGRNSYKERYLEVFRPRIKVSVLDTYQYDDGCESCQNDSFSREPAVVKFSS 120
J. Baol. Chem. 346, 7191-7200, 1971. A. D. Baol. Chem. 346, 7191-7200, 1971. A. Steference involvement of a tyrosine residue in the activity of bovine pancreatic deoxyrith, Rikeference number. A32094, MUID:72064123, PMID:5166750	QY 121 RFTEWREFAIVPLHAA-GDAVAEIDALYDVYLDVOEKWGLEDVALWGDFWAGGSIVREG 180
4, Contents: annotation 4, Note: nitration of Tyr-87 by tetranitromethane destroys a calcium binding site and ing	161 GOOTE WARRING TO THE SALVE SERVICE OF THE SALVE SERVICES OF TH
J. Mol. Biol. 221, 645-667, 1991	
4;Reference number: S19525 4;Contents: annotation; X-ray crystallography, 2.0 angstroms	Qy 241 LSDQLAQAISDHYPVEVML 259
V.Function: Description: catalyzes the hydrolysis of DNA to 5'-phosphodinucleotides and 5'-phosphodinucleotides an	Db 241 LSNEWALAISDHYPVEVTL 259
):Jugetrainly: weokylinoundigase 1 - J.Keywords: glycoprotein; hydrolase; nucleic acid degradation F:1-22/Domain: signal semimore Heraris predicted serves	RESULT 7
7/23-282/Product: deoxyribonuclease I facture experimental «MAT» 7:40/Finding site oarbohydrate (ARM) (covidatinf) #factus experimental 7:13-146,195-231/Disulifab bonds: #factus experimental	JCS31 decoyribonoclease I (EC 3.1.21.1) precursor - human N.Alternate names: DNase; thymonuclease
Query Match 78.11; Score 1067; DB 1; Length 282; Best Local Similarity 79.01; Pred. No. 1.5e-90;	Copercian October Saptems (Man) Ciperce: 10-011-1997 Heoquence_revision 29-Aug-1997 #text_change 07-May-1999 CiAccession: 105351 Heoquence_revision 129-Aug-1999 (Arc. Zhang. J.: Gentz. R.: Ruben R.28eng. Z.: Parmellee, b.: Mydw. H.; Ocleman, T.A.; Su, K.: Zhang. J.: Gentz. R.: Ruben

us-10-005-306-9.rpr

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Cybecies: Deinoscorus Tailor unclease - Deinococcus radiodurans (strain R1)
CySpecies: Deinoscorus Tailodurans e Deinococcus radiodurans (strain R1)
CySpecies: Deinococcus Tailodurans
CyAccession: D76525
CyAccession: D76525
CyAccession: D76525
CyA. M. Shen, J. A., Patedelberg, J. F. Hickey, E. K.; Peterseon, J. D.; Dodson, R. J.,
R. M.; Shen, W.; Vannelrewn, J. J.; Lam, P. W. Mononid, L.; Utterback, T.; Zalewski, C.; I.
Science 286, 1571-1877, 1999
CyA. This demonstered the radiocesistent bacterium peinococcus radiodurans R1.
A; Reference number: A7520; PAUD:2005896; PMID:10567266
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A/Mostouse (1906 DNA
A/Residuse: 1716/ AMEL)
A/Ross-reference: GB:ARD01826; NID:g6460827; PIDN:AAF12592.1; PID:g646088; TIGR:DRB
A/Roperlamental source: Entrain Rl
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Cibntes 10-Jun-1931 #sequence_revision of 3-Jun-1993 #text_change 08-Apr-1994
Cipntes 10-Jun-1993 #sequence_revision of 3-Jun-1993 #text_change 08-Apr-1994
Ridgaki, M.; Tomiyama, M.; Askutuni, T.; Hidaka, S.; Kiguchi, T.; Nagata, R.; Sato, T.
Algan, Viso, T. 72, 1497-1498 1931
A. Title: The complete monicoccie acquence of cutumber green mortle mossic virus (8H st
A. Reference number: JQ1157, MUID:91311400; PMID:1856687
                                                                                                                                                                                                                                      80 GPYSTLSSPOLGRSTYMETYVYFYRSHKTQVLSSYVYND-----EDDVFAREPFVAQFSL 134
                                                                                                                                                                                                   61 DTYHYVVSEPLGRKSYKERYLFVYRPDQVSAVDSYXYDDGCEPCGNDTFNREPAIVRFFS 120
                                                                                                                                                                                                                                                                                                                                                121 RFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                181 WSSIRLWTSPTFQWLIPDSADTTA-TPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 LGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFSRFTEVREFAI 130
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                                                     KIAAFNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQ-DAP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 RICAFNAQRITLAKVAREQVMDTLVRILARCDIMVLQEVVDSSGSAIPLLLRELNRFDGS
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Best Local Smilarity 25.74; Score 128; DB 2; Length 10
Best Local Smilarity 25.74; Pred. No. 0.0025;
Matches 46; Conservative 33; Mismatches 70; Indels
Matches 46; Conservative 33; Mismatches 70; Indels
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A. Status: Port. Interpretation of the control of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LKIAAFNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNODAP 60
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AjResdess 1-102 «PER»
AjCross-references: dS:U06846; MID:g1620035; PIDN:AAB17022.1; PID:g1620214
R. Coy. J.F.
submitted to the EMBL Data Library, July 1995
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Conchem Brophys. Res. Commun. 21, 495-564, 1897
Affitte: Cloning and characterization of a novel human DNase.
Affitte: Cloning and characterization of a novel human DNase.
Affectence number: UCSS61, MUID:97221487; PMID:9070308
Affectesign. UCSS61, MUID:97221487; PMID:9070308
Affectesign. UCSS61, MUID:97221487; PMID:9070308
Affectesign. UCSS61, MUID:97221487; PMID:9070308
Affectesign. UCSS61, MUID:97221487; PMID:9070308
CSS940CTEMIN: GeoxyThonuclease I
C,Kopyorda: Mydrolase
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F121-30s/Product: deoxyribonuclease I #status predicted <MAT>
F15S/Active site: His #status predicted
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34 0%; Score 464.5; DB 2;
Best Local Similarity 38.7%; Pred. No. 4.9e.35;
W. Cohes 10.1; Conservative 48; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                               query Match 43.2%; Score 591; DB 2; Best Local Similarity 45.2%; Pred. No. 1.1e-46; Matches 119; Conservative 51; Mismatches 89;
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C,FKPywords disulfide bond; endomuclease, hydrolase
F;57,97,48,227,365,Active site: Glu, Glu, His, Asp,
F;187-224/Disulfide bonds: #status predicted
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A.Residues 1-216 - Olls
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A.Residues 1-216 - Olls
R.Walligan - A.T. Dietrich P.S.; Hennesey, K.M.; Sehl, P.; Komp, C.; Wei, Y.; Taylor
A.Residues 1-216 - Olls
A.Residues 1-216 
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C.Reverda A7P Day repair; nuclectide binding; nucleus; P-loop; pre-mRNA splicing
FSS1-528/Region: nucleotide-binding motif A (P-loop)
F-630 615/Region: nucleotide-binding motif B
F-630 615/Region: BZM motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26
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                                                                                                                                                                                                                                                                                                       pre-mRNA splicing helicase BRR2 - yeast (Sarcharomyces cerevisiae)
Myternate names DNA repair protein RAD24; protein YER172c
C.Species: Sarcharomyces cerevisiae cerevisiae (C.Date: 28-May-1991 #sequence_revision 24-Feb-1995 #text_change 23-Mar-2001 R.Detrion, SS6675; 830856; JC4657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypotherical procein SPCC18.17c - fission yeast (Schizosaccharomyces pombe) Species Schizosaccharomyces pombe) Cybetes Schizosaccharomyces pombe Cybetes (3-10-2-1999 #sequence_sevision 01-Dec-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  931 CRNDAVNWLAYTYLYVRMLASPWLYKVPDISSDGOLKKPRESLVHSALCILKEOELVLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 TFGE----TKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLN-----
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A Mescales 1-160 - MUL
A Cross-rectedes 1-160 - MUL
A Cross-rectedes 1-160 - MUL
A Cross-rectedes 1-160 - MUL
A MARIE STATE A CROSS A CROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the BMBL Data Library, December 1994
A.Description: The sequence of S. cerevisiae cosmide 9163 and 9132
A.Merderance number: $50431
A.Mecession: $50675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 6.8%; Score 93.5; DB 2; Length 2163; BB est Local Similarity 24.8%; Pred. No.9.5; Matches 69; Conservative 30; Mismatches 86; Indels 93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1107 RILRAMFEICLKRGWGHPTRMLLNLCKSATTKWWPTNC 1144
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                                                                    714 TDYDP 718
       250 SDHYP 254
                                                                                                                                                                                                                                                  RESULT 12
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Ascretiol, 188,1986-1987, 1996
A;Tkile: Cloning, septencing, and characterization of the nucH gene encoding an extracel
A;Reference number: 220999; MUID:96272269; PMID:8682799
                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1311 SAVGOLANFINFIDLPAFÖTYMHMIKROPKSRLDISIQSEYPALGIIVYHPKVVNAVFGPV 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 -----VDS---YYYDDGCEPCGNDTFNREPAIVRFFSRFTEVREPAIVPLHAAP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 GDAVAEIDALYDVYLDVQEKWGLEDVM-----LMGDFNAGCS----YVRPSQWS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 SIRLWISPIF-----QWLIPDSADTIATPTHÇAYDRIVVAGMILRGAVVPD----SALP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 YLDVQEKWGLEDVMLMGDFNAGCSYVRPSQWSSIRLWTSPTRQWLI........... 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 ----PD--SADITATPIHCAYDRIVVAGML-LRGAVVPDSALPFNFQAAYGLSDQLAQAI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 YDDGCEPCGNDTFN----REPAIVRFFSRFTEVREFA--IVPLHAAPGDAVAEIDALYDV 150
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AiResidae: 1.100 - DDD.
AiCross-references: EMBL:176304; NID:g1185048; PID:g1185049; PIDN:AAB39273.1
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C:Species: Aeromonas hydrophila
C:Abets: 22-0ct-1399 #Sequence_revision 22-0ct-1999 #text_change 22-0ct-1999
C:Accession: T3133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46 TAVGKLLDNLNQDAP--DTY-HYVVSEPLGR----KSYKERYLFVYRPDQVSA----
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                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   71;
                                                                                                                                                                                                                                                                                                Length 1646;
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6.9%; Score 94; DB 2; Length 1070;
Best Local Similarity 20.7%; Pred. No. 3.4;
Matches 5; Conservative 38; Mismatches 90; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                   81; Indels
                                                                                                                                                                                                                                                                                 Query Match 7.4%; Score 100.5; DB 1; Best Local Similarity 22.9%; Pred. No. 1.5; Matches 56; Conservative 37; Mismatches 81;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                             C; Superfamily: cucumber mosaic virus RNA 1 protein
                                     A; Molecule type: genomic RNA
A; Residues: 1-1646 <UGA>
A; Cross-references: GB: D12505
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1533 WNFEA 1537
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A,Accession: JQ1157
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Accession: Talifo [Hilbert, H.; Dusterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G. bondreed to the EMBL Data Library, October 1998 Accession: Talifo	QY 113 PA
Status: preliminary; translated from GB/EMBL/DDBJ Joholule type: DNA Designee: 1-488 - HTT.	
/Cross-references BRELALO1907; PIDN:CAA21411.1; GSPDB:GN0068; SPDB:SPCC18.17c Cross-references Brezin 972h-; cosmid c18	CY 207 THCAYDRIVVAGHLIRGANVPDSALPRHEGLSDQL 245  Db 565 GHCLLLGIFFRANSVARRL 595
dens. SpBus. 2007.018.17c  Map position: 3  Superfamily: Schizosaccharomyces pombe hypothetical protein SPCC18.17c	RSSUT 15
Query Match 6.78; Score 91; DB 2; Length 488; Merches deet Local Similarity 21, 77 Pred, No. 2.2; Matches 4; Conservative 4; Mismatches 91; Indels 98; Gaps 13;	Nazae, GDXG family VCA0490 [imported] - Vibrio cholerae (strain N16961 serogroup 01) Cispecies 'Whito cholerae Cispecies 'Naza-2000 Respence_revision 20-Aug-2000 Htext_change 02-Feb-2001
y 10 regetronsharivsylvolleryolalvoevroshiranoklidalalo 57 1.73 fvodelariavbaltleratiseseskeselikodlulrodnedilo.222	Cyrocesson; G87435 Esten, J.A.; Nelson, W.C.; Clayton, R.A.; Gainn, W.L.; Dodson, R.J. Chardenberg, J.F.; Effoldeav, D.; Vometherwin, J.; Base, S.; Qin, H.; Dragoi, I.; Sellers, J. R.R.; Wekhanos, J.J.; Venter, J.C.; Fraeer, C.M.
y 58DAPDTYHYVVSEPLGRKSYKERYLEVYREPQVSAVOSYTYDDGCEPCSHDTENREPA 114  233 INLAR-PTF1111	Nature 40%, 477-7853, 2000 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A;Reference number: A82035, WUID:20406833, PMID:10953301 A;Accession: G82453
y 115 IVRFFSRFIEVRERIVDHAAPG-DANAEIDALUDVIDVORK 157 b 272	A.Stetus: przed_iminary A.Molecule type: DNA A.Residues: 1.337 -HELT. A.Cross-teterences: GB.AR.004380, GB.AR.003853, NID:99657884, PIDN:AAF96394.1, GSPDB:GNO
y 158 WGLEDVMLAH-GDFWAGCSYVREGWSSIRLWTSFTEGWLFDSADT 202  331 YGLEDGRANFYVPRHITMRF[NDEDGMSSRANALADGUHLAMGLAHILPDFTLS 384	A.Experimental source: serogroup Ol; strain Ni6961; biotype El Tor C;Genetics: A.Gene: VGA0490 A.Map position: 2
Y 203 TATPTECAYDRIVAGAVVEDSALPFNFQAAYGLSDQLAQAISDHFPVBV 257  385 TLVAY	Query Match 6.6%; Score 90; DB 2; Length 337; Best Local Similarity 24.2%; Par No. 1.7; Batches 67; Conservative 38; Mismatches 102; Indels 70; Gaps 15;
BB36 BB36	QY 1 LKIARINIQFRGETXMSNATUNSYIVQILSRYDIALVQEVROSHLTAVGKLIDNIANDAP 60  18
Special cas process arXiv: Lagories 1, Naporces 1 - Nosico 59, (Britain PCC 7120) 75pecies Nosicos 5p. PCC 7120 is a synonym of Anabaena 82 strain PCC 7120 is a synonym of Anabaena 82 strain PCC 7120 is 1970-1970	CY 61 DYMYTVVBEPLGRKSYKERYLPVYRP-DQVSAVDDSYYXDDGCEPCGNDFF 109  64 RRACHISTAGSSPRAAGSSPRAADSPUBLIGGTOWN/WEGEKTIDFTTYPHGGCFF 21
Kanesson: Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watenabe, A.; Iriguch; Makazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yamuda, M.; Tabata, S. Na Res. 8, 205-213, 2001. Aftle Complete Ganouic Sequence of the Filamentous Mixrogen-fixing Cyanobacterium And	QY 110 NREPAIVRFFSRFTEVREFAIVDLAARGDANAELDALYDVYLDVQEKMGL 160 Db 122 ETHBAQLKQLAHLSFTIVVCIKYRLAPEHAYPSAHDOVPQAALGIKEHGHKYGGDT 177
Seference under: AB1807; MUID:21595285; PMID:1175940 Accession: AB1848 Accession: AB1848 Accession: AB1848	CV 16.1 EDVMANGENAGENARPS-OWENETHEATSTTFOWIL
.Residues: 17-61 -KUR>. Close-references: GB:BA000019; PIDN:BAB72289.1; PID:g17129676; GSPDB:GN00179 -Experimental source: strain PCC 7120 -Forestics: 100-1031.	OY 210 AYDRIVVAGMILRGAVVPDSALPRPQAAYGLSDQIA 246
Query Match 6.7h; Score 91; DB 2; Length 761; Matches 60; Conservative 38; Mismatches 97; Indels 84; Gaps 13;	Search completed: November 21, 2003, 13:57:08 Job time : 23 secs
10 TEGETONSNATLVSYIVQILSRYDIALVQEVRDSHLTANGGLIDNLAQDAPDT 62 348 TAGQTLALTREITAETHÄLLAKAQKAGKHEDĞRRSAGĞKILBERLGENARQEPHT 404	
63 YHYVWSBPLGRKSYKERYLFVYRPDQVSAVDSYYDDGCGFGGNGFRRE 112 b 495 PYYGYUDAPPLAJANISSPYSRYHERTLEGLMANIAAMGWIDSWADGYYTVUDV 4.6.9	

us-10-005-306-9.rsp

## GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

November 21, 2003, 13:45:00 ; Search time 17 Seconds (Without alignments) (Without alignments) 719:232 Willion cell updates/sec Run on:

US-10-005-306-9 1367APRIQTFGETKMSNAT......LSDQLAQAISDHYPVEVMLK 260 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched: Total number of hits satisfying chosen parameters:

127863

Minimum DB seq length; 0 Maximum DB seq length; 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result baing printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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encodes an Azg to Cys substitution responsible for its instablicy.";
Blochem. Biophys. Res. Commun. 260:362 3311999.

Blochem. Biophys. Res. Commun. 260:362 3311999.

DEATH BY APPOTOSIS BINDS SPECIFICALY TO G-ACTIN AND BLOCKS.
ACTIN HOVENSTEAMTON (BY SIMILARITY).

C. CATALYTIC ACTIVITY: BROMUCLEOLYTC is cleavage to 5'-
phosphodimolecide and S'-phosphodisgouncleotide end-products.

C. CORACONS DIVERRY CATYONS, PROTEINS YOURD IN STORED
ESTABLIAR LOCATION: SECRETORY PROTEINS. TORRE IN STORES

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WENDLINE-2551715; PubMed-7525762;

WENDLINE-2551715; PubMed-7525762;

WENDLINE-2551715; Number D., Takeshita H., Tenjo E., Kishi K.;

"Molecular analysis of the third allele of human deoxyribonuclease I
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Barton R.W., Fazina P.R., Satina P.R., Asaina P.R., Ash Mann urine-derived interleukin 1 inhibitor. Homology with
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Blob W. Asatud: T. Aoyama M., Tsubota E., Kobayashi M., Yuasa I.,
Metubii T. Kishi K. Aoyama M., Tsubota E., Kobayashi M., Yuasa I.,
"The fifth allele of the human deoxyribonuclease I (DNase I)
                                                                                                                                                                                                                                                                                                                               human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Slectrophoresis 18:1936-1939(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=89035996; PubMed=3263467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polymorphism.";
Ann. Hum. Genet. 59:139-147(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               deoxyribonuclease I.";
J. Exp. Med. 168:1767-1779(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Urine,
MEDLINE=91115785, PubMed=2277032;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 23-45 AND 73-95.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 23-49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT DNASE1*6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polymorphism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Urine;
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NOTE=Clinical information on Pulmozyme; WMWe="http://www.genentech.com/gene/products/information/opportunistic/pulmozy This SWISS-PROT entry is copyright. It is produced through a collaboration the wash institute of Bioinformatics at the Biological cuttation. There are no testrictions on tis the biological miscinicions in the biological content in the biological content is not profit institutions as longs as its content is in no way mettified and this scatement is not removed. Wellow the and for connectal entries requires a license agreement (see http://www.isp-sib.ch/announce/or send a mail to licensesiab-sib.ch). ö 61 DIYHYVVSEPLGRKSYKERYLFVYRDDQVSAVDSYYYDDGCEPCGNDTRNREPAIVRPFS 120 1 LKIAAFNIQTFGETKASNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNINQDAP 60 23 LKIAAFNIQTPGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAP 82 Name Accounts of the Account of the 0, Gaps DISEASE: DNASE PHENOTYPES HAVE BEEN SHOWN TO BE ASSOCIATED WITH PRAME/CENTICAL Available under the name Pulmogyue (Genentech).
 Used to reduces the viscosity of cystic fibrosis spurum by hydrolysing the extracellular DNs. released by degenerating leukocytes that accumulate in response to infection.
 STATILARTY: SERONGS TO THE DNASE I FAMILY.
 DATABASE: NAME-Pulmosyme; N-LINKED (GLCNAC, .). (POTENTIAL). Q -> E (in allele DNASE1\*4). BY SIMILARITY.
ESSENTIAL FOR ENZYMATIC ACTIVITY
(BY SIMILARITY). Length 282; /FTId=VAR 002264. V -> M (in allele DNASE1\*5). /FTId=VAR\_009300. /FIId=VAR\_002265. R -> C (in allele DNASE1\*6). Indels P -> A (in allele DNASE1\*3; /FTId=VAR 002266. L -> H (IN REF. 2). 040042E2D23555B6 CRC64; DEOXYRIBONUCLEASE I. Score 1362; DB 1; 1.6e-120; /FTId=VAR\_009301. R -> Q (in allele dbSNP:1053874). BY SIMILARITY BY SIMILARITY 0, Mismatches Pred. No. EMBL, M55983, AAA63170.1, -.
EMBL, D83195, BAA1841.1; -.
EMBL, AC062603, AAC24721.1; -.
EMBL, AJ298844; CAC12813.1; -.
EMBL, BC029437, AAH29437.1; -. 282 AA; 31433 MW; 99.64; PIR; A38417; NDHU1. HSSP; P00639; 3DNI. Genew; HGNC:2956; DNASEI. Best Local Similarity 99.6 Matches 259; Conservative 100 126 207 154 244 23 123 100 40 128 31 154 207 244 DISULFID ACT\_SITE CARBOHYD CARBOHYD SEQUENCE ACT SITE CONFLICT Query Match /ARIANT /ARIANT VARIANT PARIANT VARIANT CHAIN + 

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This SWISG-ROY entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the BUBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as the content, is, in no way modified and this extendent is not removed. Usage by and for connectial entities requires a license agreement (See http://www.isb-sib.ch/announce/or sent an email to licensestable.ch/announce/
                                                                                                                                                                                        181 WSSIRLWISPTFQWLIPDSADTTATPTHCAYDRIVVAGWLLRGAVVPDSALPFNFQAAYG 240
83 DTYHYVVSEPLGRNSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 142
                                                             121 RFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPSQ 180
                                                                                                 203 WSSIRLWTSFTFGWLIPDSADTTATFTWCAYDRIVVAGMLLRGAVVPDSALPFWFGAAXG 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REDLINE-SIGOTAR, PHORE-SPECIAL TRANSPORT AT THE ACTION OF A THE ACTION OF A THREATH M. French M.E., Trachopp J.; Green M. French M. Fren
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takeshita H., Yasuda T., Nakajima T., Hosomi O., Nakashima Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dibil. 100182 STANDARD;
10.1782-1596 [Rel.] 3.0, Created)
10.1782-1596 [Rel.] 3.0, Created)
10.1782-2096 [Rel.] 3.6, Last sequence update)
10.4047-2000 [Rel.] 3.6, Last sequence update]
10.5047-2000 [Rel.] 3.9, Last sequence [Rel.] 3.1048-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-BALB/G. TISSUE-Kidney, and Parotid gland,
MOLLINE-9735420; PubMed-9192086;
                                                                                                                                                                                                                                                                                                                        241 LSDQLAQAISDHYPVEVMLK 260
                                                                                                                                                                                                                                                                                                                                                                                263 isboladaisbhyrvevalk 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U00478; AAA03710.1; -. EMBL; D83038; BAA28622.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BALB/c; TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JC2526; JC2526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNASE1 OR DNL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
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HSSP, P00619; JDNI.
MGD, WGI.103157; Dnasel.
InterPro; IPR001182; DNase I.
InterPro; IPR005115; Exo\_endo\_phos.
Pfan; PP033175; Exo\_endo\_phos; OFANYS; PR0119; DNASEI.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 RFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPSQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Bakaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bakaryota, Butharia, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBL TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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HEDLINES-Sprages—Duelpy;
HEDLINES-Sprages—Duelp
Procort PROMOGAG Names.C. 17.
PROCHER, PROMOGAG NAMES.C. 27.
PROCHER, PROMOGAG NAMES.C. 27.
PROCHER, PROMOGAG NAMES.C. 27.
PRACTICE, PROMOGAG NAMES.C. 27.
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PRACTICE, PROMOGAG NAMES.C. 27.
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N-LINKED (GLONG. . .) (POTENTIAL)
N-LINKED (GLONG. . .) (POTENTIAL)
AG -> VR (IN RRF. 1).
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HEDRINGS-9108312; PubMed-226.3485;
POUR-26-16 HEDRINGT H.G. FAIL I BRIGHT CONN. CLONE CHOCKEN
POUR-26-16 SEQUENCE OF A FAIL I BRIGHT CONN. CLONE ENCODING THE
NUCLEC ASSAURT CONN. CLONE SEE I From the rat payor to the condition of the control of the c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82,3%; Pred. No. 1.45-37;
Live 23; Mismatches 23; Indels
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239 240 AG -> VR (IN REF. 1).
284 AA, 32027 MW, 8682E20515EEB510 CRC64;
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01-NAY-1991 [Rel. 18] last sequence update)
16-07-2001 [Rel. 18] last sequence update)
16-07-2001 [Rel. 40, last annotation update)
18-08-yribonuclease I precursor (EC 3.1.21.1) (UNase I).
1878-EI OR DRIL.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DIYHYVVSEPLGRKSYXERYLPVYRPDQVSAVDSYYYDDGCEPCGNDIPWREPAIVRPFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 RFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKAGLEDVALAGDFNAGCSYVRPSQ 180
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PROSTER, PROSOJS, DAMSE 1.1, 1.
PROSTER, PROSOJS, DAMSE 1.2, 1.
PROSTER, PROSOJS, DAMSE 1.2, 1.
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ESSENTIAL FOR BIZZMAZIC ACTIVITY
(BY SIMILARITY)
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N-LINEED (GLCHAC. . ) (POTENTIAL)
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128 128 N-LINKED (GLCNAC. . .) (PC
284 AA; 32064 MM; 45075AFF133781FA CRC64;
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tive 29; Mismatches 22
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EMBL, U76635, AAB71495.1; -.
PIR, S13676; S13676.
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InterPro. PRO01515; Exc endo_phos.
The Harm Pro1372; Exc endo_phos.
PRANTS; PRO0130; DNS.EX.
ProDom; PD005468; DNS.EX.
ProDom; PD005468; DNS.EX.
Prop. Prop. Prov.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 LINOMAEAISDHYPVEVTLR 282
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INVOLVEMENT IN APOPTOSIS
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This SWISS-BAT entry is copyright. It is produced through a collaboration between the Swis Tractivue or Swisinformatica and the DWG outstation the Envelopen Bioinformatics Institute. There are no restrictions on its use by non-popul shortcuttunes as to so its content is in no way modified and this statement is now removed. Usage by and for commercial entities requires a literate system (See http://www.isb-sb.ch/announce/or send an east to iterase(sb-sb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLOGHER 1. J. 1318-185-141(1997).

IN STRUCTION, ANNOG COTER PURCTIONS, SERNS TO BE INVOLVED IN CELL.

I. SHUCTION: ANNOG COTER PURCTIONS, SERNS TO G.ACTIN AND BLOCKS ACTIN

BLOWING THE A AROPICASIE, BLINDS SERVEN COS DOUBLE-STRANDED DN. AND

PRODUCES OLICONOLICACIOLES WITH 5'- PROSEND AND 3'- HUPROKY TERMIN.

CATALYTIC ACTIVITY: ENGENCY CALCARY CALCARY ON 3'- HUPROKY TERMIN.

I. COPACIVE: DIVALENY CATIONS, PROFERI, SYGNED IN SERVESSE ASMALLES AND CADOLOGY, STORESTON STORESTON, STORESTON STO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protecochemical characterization, nucleotide sequence, expression in
stateuce, relationships with other mammalian DNsees I and phylogenetic
attatuse, relationships with other mammalian DNsees I and phylogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- SIMILARITY: BELONGS TO THE DNASE I FAMILY.
                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Makaryota, Mecazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, lagomorpha, Leporidae, Oryctolagus.
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PROSITE; PS00918; DNASE I 2; PALSE NEG.
Hydrolaes; Endontclease; Nuclease; Glycoprotein; Calcium; Signal;
Apoptoslas; Actin-Chinding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      asuda T., Takeshita H., Nakajima T., Hosomi O., Nakashima Y.,
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., SEQUENCE OF 22-41, AND CHARACTERIZATION STRAIN-adaptes white of TISSAIN-adaptes and Utine; STRAIN-adaptes with PubMed-9230,129,
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281 AA, 31345 MW, 6B6535FCE1FE29E8 CRC64;
                                                                                                               15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last amocation update)
Booyvribonuclease I precursor (EC 3.1.21.1) (DNase I).
DNASEL OR DNIL.
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HSEEP, DEGRET BALLZTALI, -
HSEEP, DEGRET BALLSTALI, -
INTERFOR, DEFOLISE, DANSER, L
INTERFOR, DEFORES, EXO-emico, pho-
PRINTE, PRODIJO, DANSER,
PRINTE, PRODIJO, DANSER,
SHART, SAGONTO, BALLSTAL
                                                                                      15-DEC-1998 (Rel. 37, Created)
                            STANDARD;
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                            DRNI RABIT
018998;
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ACT SITE
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DRN1 RABIT
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81.64; Score 1116, DB 1; Length 281;

Best Local Similarity 82.2%; Pred. No. 2.1e-97; Matches 213; Conservative 22; Mismatches 24;

Query Match

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                                                                                                                                                                                                                                                                                            61 NNYHHVVSEPLGRSTYKERYLFVPRPRQVSVLDSYLYDDGCEPCGNDTFNREPSVVKFSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                          PFTQVKEPAIVPLHAAPSDAAAEINSLYDVYLNVRQKWDLQDIMLMGDFNAGCSYVTTSH 180
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                                                                                                                                              MEDLINE-73149229; PubMed=4735137;
Salnikow J., Murphy D., Ti
TBOVIne pancrealic deoxylbonucleases A and C. A proline for histidine
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Liso T.-H. Salnikow J., Noore B., Stein M.H.;
strict parcreatic decayribonuciaes A. Isolarion of cyanogen bromide epsiles promplee ovalant serroute of the polypeptide chain.";
J. Biol. them. Zela:1489-1495(1973).
                                                                                                           1 LKIAAPNIQTFGETKWSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAP
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Mammala, Butherria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Boyldae, Boyldae, Bos.
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     ilarity 77.3%; Pred. No. 2.6e-93;
Conservative 30; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121-UU-1986 (Rel. 01, Created)
IL-DEC-1998 (Rel. 17) Last sequence update)
28-F82-2003 (Rel. 41, Last annotation update)
Bescyribonuclases I precursor (EC 3.1.21.1) (DNase I)
NNASEL OR DNIL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Stein W.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             282 AA.
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"Bovine pancreatic deoxyribonuclease D.";
J. Biol, Chem. 249;2354-2356(1974).
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J. Biol. Chem. 248:1499-1501(1973).
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Liao T.-H., Salnikow J., Moore S.,
J. Biol. Chem. 267:7957-7957(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 LSDQLAQAISDHYPVEVMLK 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Best Local Similarity
Matches 201; Conserv
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1. FUNCTION: ANNOS OTHER FUNCTIONS; SERBS TO BE INVOLVED IN CELL. PROCRIME IN A PROCROSIG. BINNOS SERBS TO G. ACTIN AND BLOCKS.

1. FUNCTION: ANNOS OTHER FUNCTIONS; SERBS TO G. ACTIN AND BLOCKS.

1. FUNCTION: ANNOS OTHER FUNCTIONS; SERBS TO G. ACTIN AND BLOCKS.

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     1 LKIAARNIQTEGERKKSNAFLYSYIVQILSRYDALVQBYRDSHLTAVGKLEDNIAQDAP 60
22 LKIAARNISSEGERKOSNAFLTSYIVRIQRYDALQGYRDSHLTAVGKLEDKLAKARA 81
22 LKIAARNISSEGERKOSNAFLTSYIVRIQRYDALQGYRDSHLTAVGKLEDKLAKARA 8
                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
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SMART; SMOO476; DMase_In; 1.
PROSTE; PS00914; DMASE_In; 1.
PMCO178; PS00914; DMASE_In; 1.
PMCO178; PS00914; DMASE_In; 1.
PMCO1889; Enfontuclease; McOtesse, Glycoprocein; Calcium;
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01-007-1999 (Rel. 12, Last sequence update)
01-NOV-1997 (Rel. 13, Last sequence update)
00-NOV-1997 (Rel. 13, Last samotarion update)
DANSEL OR DNI.1.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
BMBL; AJ001538; CAA04819.1;
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NITRATION BY TETRANITROMETHANE DESTROYS
A CA++ BINDING SITE & INACTIVATES ENZYME.
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78.1%; Score 1067; DB 1; Length 282;
Bast Local Sfailarity 78.0%; Pred. Nb. 8.38-93;
Watches 202; Conservative 28; Wisharches 29; Indels 0
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INVOLVED IN ACTIN-BINDING.
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               This SHISS-PROT entry is copyright. It is produced through a collaboration between the Savies Institute of Bioinformatics and the Bubl outsettion the Ruscopen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this estrement is not removed. Usage by and for commercial
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*** STATE OF THE ACTION OF THE
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Suck D. Officer: 0. Officer: 1 at 2.0-A resolution suggests a mechanism for binding to and cutting DMN.;
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Black State Conditions DMN.;
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                                      WEDLINE=69184134; PubNed=4976790;
THICE P.A., MOONE 95, SEATH W.H.,
"Alkylation of a histidiae residue at the active site of bovine
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MEDLINE-23389259, PubMed-1518054;
MKGLINE-23389259, PubMed-1518054;
MK-ray structure of the DNase I-d(GGTATACC)2 complex at 2.3-A
                                                                                                                                                                                              WEDLINE-17264723; PubMed-5166750, WEDLINE-17264723; PubMed-5166750, PubMed-1914 T. PubMed-1914 T. PubMed-1914 T. PubMed-1914 G. a Lyrosine residue in the activity of bovine resurce to decyrizbonuclase A. J. S. Asol. Chem. 246; 7191-7200(1971).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2 ANGSTROMS).
MEDLINE=92085280; PubMed=1748997;
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MEDLINE=87169744; PubMed=3560229;
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J. Biol. Chem. 244:924-928(1969).
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J. Mol. Biol. 226:1237-1256(1992)
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InterPro, IPR005135; Exc_endo_phos.
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Best Local Similarity
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23 LKTAARNIFFGEFCASNAFLASYIVRIVRYDYJLLQGVRDSHLVAVGKLLDYLAQDOP 82
24 LKTAARNIFFGEFCASNAFLASYIVRYDYNLQGVRDSHLVAVGKLLDYLAQDOP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ovis aries (Sheep).

Bokaryota (Netebrata; Chordata; Craniata; Vertebrata; Eutoleostoml;
Mommalia; Eutheria; Cetatiodactyla; Ruminantia; Pecora; Bovoidea;
Povidea, Captinea; Ovia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESSENTIAL FOR ENZYMATIC ACTIVITY (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1989 (Rel. 12, created)
01-0CT-1989 (Rel. 12, hast sequence update)
01-NOY-1997 (Rel. 35, Last annotation update)
beoxyribonuclease I (EC 3.1.21.1) (DNase I).
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87057261; PubMed=3782105;
                                                                                                                                                                                                                                                                                                   241 LSDQLAQAISDHYPVEVML 259
                                                                                                                                                                                                                                                                                                                         263 LSNEMALAISDHYPVEVTL 281
                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                       DRN1 SHEEP
P11937;
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ACT_SITE
CARBOHYD
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-1- SINGLARIY: BELONGS TO THE DIAGE. I PAMILY.
-1- SINGLARIY: BELONGS TO THE DIAGE. I PAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 RFTEVRERATOPLARAPGDANARIDALYDVYLDVORKWGLDVVAMCDFVAGCSYVRSQ 180
121 FSTKVARATYVPLASABEDANARISSLYDVYLDVORMUNDINITAMODENDGCSYVRSQ 180
121 FSTKVARATYVPLASABEDANARISSLYDVYLDVORMUNDINITAMODENDGCSYVRSG 180
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DTYHYVVSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 WSSIRLWISPIFQWLIPDSADITATPIHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAYG 240
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                                                                                                                                                                                                                                                                                                                        1 LKIAAFNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAP 60
                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DE-1398) to the BRGING-BRAN/DRAI databases.

-- INDEXTH WARDONG OTHER PROFITORS. SERVE TO BE INVOLVED IN CELL
DEATH WARDONGS IS BINDS SERVETCALLY TO G-ACTIN AND BLOCKS ACTIN
PROMINETARION (BY SIMILARITY) CALCING AND BLOCKS ACTIN
PURPORADIAL CHECKE and 5 - "DEPRIDENDIAL SHOWLE SELVE SHOW SHOWLE SHOW AND SHOULE SHOWLE SHOW SHOWLE SHOW SHOWLE SHOWLE SHOW SHOWLE S
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Bukazyota Metazoa Chordata, Craniata, Vertebrata, Euteleostomi,
Artoosauria, Nves; Neogharhae, Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in S.C. Hu C.C., Liao T.H.;
"Chicken pencerated decoyribonuclease I: purification and
characterization as well as cloning, sequence and expression of its
Ouery Match 77.6%; Score 1061; DB 1; Length 260; Best Local Similarity 77.2%; Pred. No. 2.76-92; Matches 27; Indels (Matches 20); Conservative 32; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
Locyt-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Deoxyribonuclease I precursor (EC 3.1.21.1) (DNase I).
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SEERES SELECTEREES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HissP: poto59; JNN 1000 JNN 10
                                - SIBDATI, NOCOMEAT.

- SIBCALLIARA LOCATION SECRETORY PROTEIN, STORED IN ZVMOSEN GARALLES MAD FOUND IN THE MICLEAR ENVELOPE (BY SIMILARITY).

- MISCELLANGOUS. MOST ACTIVE AT PH 9.5.

- SIMILARITY, BELONGS TO THE DNASE I PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.8%; Score 736; DB 1; Length 284;
54.8%; Pred. No. 1e-61;
ive 44; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32215 MW; D5154AF0C782B595 CRC64;
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01.-XVV-1997 (Rel. 35, Last sequence update)
101.-XVV-1997 (Rel. 42, Last annotation update)
101.-XSP-2103 (Rel. 42, Last annotation update)
101.-XSP-2103 (Rel. 42, Last annotation update)
101.-XSP-2103 (Rel. 42, Lest annotation update)
101.-XSP-2103 (Rel. 42, Lest annotation update)
101.-XSP-2103 (Rel. 42, Lest annotation update)
101.-XSP-2103 (Rel. 43, Lest annotation update)
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BY SIMILARITY.
N-LINKED (GLCNAC. . .).
      WHICH HAVE A SYNERGISTIC EFFECT ON ACTIVATION.
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Matches 142; Conservative
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284 AA;
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I. PINCTICALIA, AWANG OTHER PRINCIPORS. SEEMS TO BE INVOLVED IN CELL.

IDENTIFY A ROPPOUSE, BINDS SPECIFICALIAT FOR SACTINA DELICACES ACTIN BECURES CALICAMICATORIAN SPIRES SACTINA STATINA STRACES DOUBLE-STRANDED DNA AND PRODUCES CALICAMICATORIO SPIRES THAT S. PROPED NO. 9. "HYDROXY TERMINI. PROGRAMMACH CALE AND STATINATICAL CALENDED COST. OF "PROPED STATINATION OF THE STATINATION OF THE STATINATION OF THE STATINATION OF THE STATINATION AND MAGNESIUM.

-1. CORPACIONE. DIVALENT CATINGS, PARTICULARLY CALCIUM AND MAGNESIUM.
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PROSITE: P800919; DWARE 1.2; 1.1
PROSITE: P800919; DWARE 1.2; 1.1
PROSITE: P800919; DWARE 1.2; 1.2
Apoptosis; Actin-binding.
POTENTIAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SINILARIY)

154 154 BY SIMILARIY

158 154 BY SIMILARIY

158 154 BY SIMILARIY

158 154 BY SIMILARIY

158 225 AAJ 31400 WM; 2256757869842BA7 GCG64;
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ESSENTIAL FOR ENZYMATIC ACTIVITY
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MEDLINE-98055705, PubMed-9395337,
Haiao Y.-W., Ho H.-C., Wang W.-Y., Tam W.P., Liao T.-H.,
Haiao Y.-W., Ho H.-C., Wang W.-Y., Tam W.P., Liao T.-H.,
mosambicus) decoyribonuclease I. Primary structure and ORNA
mosambicus) decoyribonuclease I. Primary structure and ORNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., SEQUENCE OF 27-284, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.7%; Score 762; DB 1; Length 282;
llarity 58.1%; Pred. No. 3.6e-64;
Conservative 34; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                       DEOXYRIBONUCLEASE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 284 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 LSDQLAQAISDHYPVEVMLK 260
Pfam; PF03372; Exo endo phos; 1.
PRINYE; PR00120; DNASEI.
Propom; PD005408; DNASEI.
SWART; SW00476; DNASEIC; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cichlidae, Oreochromis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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OREMO

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2; Gaps

DNAryota, Metazoa, Chordata, Craniata; Vertebrata, Euceleostomi; Memmalia, Eutheria; Primates; Catarrhini; Hominidae, Homo. NOB\_TaxID=9606;

Homo sapiens (Human)

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DNASELL3.
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                                                                                                                                                                                                                           A NEULIME-213925-7; FUDNEST-14/1/121, CECURE D.H., DETGE J.G., STRANGER S.L., SURGERE T.R., SURGERE C.R., SEMILE G.D., STRANGER S.L., SURGERE C.R., SEMILE G.D., STRANGER S.L., SURGERE C.R., SEMILE G.D., SURGERE G. C.R., SEMILE G.D., SURGERE G. C.R., SEMILE G.D., STRANGER S.F., SURGERE G. C.R., SEMILE S. S. SURGERE S.F., PROFESSER, A.P., REIDE G.M., SIGHELT T.S., SEPRILE G.G., SERCHMERCEN M.S., SORTER A.A., REINTHING P. PROFESSER, S.L., LOGGER S.M., PREERS G.J., ADTAGRSON R.D., MAILIANG S.J., SERCHMERCEN S.A., COMPANIED P.H., STRANGER S.A., MORIJA K.C., Hale S., Garcia A.M., Gay L.J., Hally S.M., WILLIAMON D.M., SOGREGER S.J., ADTAGRSON R.D., MAILIANG S.J., MAILIAMON A.S., MORIZON K.C., Hale S., Garcia A.M., Gay L.J., Hally S.M., WALLY S.M., WALLANGER S., WORLD A.C., SOGREGER S.J., LOGGER S.J., SOGREGER S.J., LOGGER S.J., SOGREGER S.J., SOGREGER S.J., SOGREGER S.J., SOGREGER S.J., SOGREGER S.M., SOGREGER S.M., SOGREGER S.M., SOGREGER S.M., SOGREGER S.M., SOGREGER S.M., SAGREGER S.M.
DNASE I HOMOLOG PROTEIN DHP1.
BSSENTIAL FOR ENZYMATIC ACTIVITY
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIN 60552; ...
Obj. 00:000556; F:calcium ion binding activity; TAS.
Obj. 00:000556; F:calcium ion binding activity; TAS.
INTERFOR INTERCATED TO THE CONTROL OF T
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BY SIMILARITY
                                                                                                                                                                                                                 MEDLINE=22388257; PubMed=12477932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BC035205; AAH35205.1; -. HSSP; P00639; 2DNJ. Genew; HGNC:2958; DNASE1L2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 AA; 32853 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51,1%;
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SEQUENCE
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                                                                       82 HEYSEVGSQPLGEDQYKEMYLFUYRKDANGVVDTYLYPD-----PEDVFSREPFVVKFSA 136
                                                                                                                                                                                                                                                                                                                           61 DIYHYVVSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120
                                                                                                                                                                                                                                          (21 RFTEVR--------EFAIVPLHAAPGDAVABIDALYDVYLDVOEKWGL 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 EDVALAGDFNAGCSYVRPSQWSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGML 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R WED, WGITILIGATE, Threadless, TAMES, CONTROLOGSE4, CINCLESS, TAMES, TO CONTROLOGSE4, CINCLESS, TAMES, TO CONTROLOGSE4, CINCLESS, TRANSPORTER, PERMEDANCIESS, PERMEDANCIESS, PERMEDANCIESS, PERMEDANCIESS, PROPERCIEST, DANSE, TREPERCO, TREOLOGSE3, PRACE, DANSE, TREPERCO, TREOLOGSE3, DANSE, TAMES, PRODUSTS, RACE AND CONTROLOGSES, CALCIUM, SIGNAL, NUCLEAR PRODUSTS, PROCESTES, PROGRAM, SECTION, CALCIUM, SIGNAL, NUCLEAR PROCESTES, PROCESTES, CONTROLOGSES, CALCIUM, SIGNAL, NUCLEAR PROCESTES, PROCESTES, CONTROLOGSES, CALCIUM, SIGNAL, NUCLEAR PROCESTES, PROCESTES, CALCIUM, SIGNAL, NUCLEAR PROCESTES, CALCULAR, NUCLEAR PROCESTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-08C-1998 (Rel. 77, Ceacache
19-08C-1998 (Rel. 77, Last sequence update)
30-MX-2000 (Rel.) 39, Last amonetion update)
Booxytibonuclease gamma precureor (EG 31.121.) (DNAse gamma)
(Deoxytibonuclease gamma precureor (EG 31.121.)
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Bukaryota, Metazoa (Chordata) Craniata, Vertebrata, Euteleostomi;
Bammalia, Eutheria, Kodentia, Sciurognathi, Muridae, Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221 LRGAVVPDSALPPNFQAAYGLSDQLAQAISDHYPVEVMLK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 LRRSLKPQSATVHDFQBEFGLDQTQALAISDHFPVEVTLK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 310 AA.
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O55070;
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SIGNAL
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BY SIMILARITY.

52

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74; Indels 25; Gaps

38, Mismatches

Matches 143, Conservative

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1 LKIAARNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAP 60  us-10-005-306-9.rsp

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26 LRLCSFNVRSFGESKKENHNAMDIIVKIIKRCDLILLMEIKDSNNNICPMLMEKLNGNSR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LKIAAFNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNINQDA- 59
Arch. Biochem. Biophys. 346:15-20(1997).
                                                                                                                       chymocytes."
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SIGNAL
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                                                                                                                                                                                 FUNCTION,
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                                                                                                                                                                                                                                                                                                                                                                                     179 SOMSSIRLWISPIFOWLIPDSADTIA-TPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 PSRFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLBDVMLMGDFNAGCSYVRP 178
                                                                                                                                                                                                                                                                                 LKIAAFNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDA- 59
                                                                                                                                                                                                                                                                                                        26 LRLCSFNVRSFGASKKENHBAMDIIVKIIKRCDLILLMEIKDSSNNICPMLMEKLNGNSR 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sporprace provin N.a., and CHARACTERIZATION.

REDLINE-Sprague-Dawley, TISSEE-Liver;
LNEDLINE-Sprague-Dawley, TISSEE-Liver;
LNEDLINE-Sprague-Dawley, TISSEE-Liver;
LNEDLINE-Sprague-Dawley, S., Shingh R.K., Lin M., Ribecco M.,
Borowy-Borowski H., snin Lb B., Lebbland J., Walker P.R., Sikorski M.,
Borowy-Borowski H., snin Lb B., Lebbland J., Walker P.R., Sikorski M.,
Propowy-Borowski H., snin Lb B., Lebbland J., Walker P.R., Sikorski M.,
Borowy-Borowski H., snin Lb B., Lebbland J., Walker P.R., Sikorski M.,
Propowy-Borowski H., snin Lb B., Lebbland J., Walker P.R., Sikorski M.,
Borowy-Borowski H., snin Lb B., Childhand J., Shorski M.,
Borowy-Borowski H., snin Lb B., Shorski M., Shorski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRatus morgajusa (Ravogiusa (Ravogiusa (Ravogiusa))
Mommalias Butheria, Rodentias Sciurognathi, Muridae; Murinae; Rattus
(Parizatiosiolia)
                                                                                                                                                                                                                                           4, Gaps
                                                          NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
ESSENTIAL FOR ENZYMATIC ACTIVITY
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PUNIZINE-STATES).
PUNIZINGENTO, I Lwamateun A., Tamma S.-I.;
Punizinearion, charactexization, and amino acid sequencing of DNase
gamma from tet splean.';
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shickewa D. Tannam S. Tannam S. Tannam S. Tannam S. Wolecular clonding and expression of a cDNA encoding an apoptotic endonuclease DNace gamman. T. ...
DEOXYRIBONUCLEASE GAMMA,
BIPARTITE NUCLEAR LOCALIZATION SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70-6AX-2000 (Rel. 19, Created)
30-ABX-2000 (Rel. 19, Last sequence update)
28-FSB-2003 (Rel. 41, Last atmocation update)
28-FSB-2003 (Rel. 41, Last atmocation update)
(Decoyribconuclesse gamma Precursor (IS 3.1.21.-) (DNase gamma)
(Decoyribconuclease 1-11ke 3) (DNase1).
                                                                                                                                                                                                 Length 310;
                                                                                                                                                                                                 44.0%; Score 601; DB 1; Length 310
46.4%; Pred. No. 5.4e-49;
tive 45; Mismatches 92; Indels
                                                                                                                                                             BE483821E045E374 CRC64;
                                                                                                (BY SIMILARITY).
BY SIMILARITY.
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STRAIN=Sprague-Dawley, TISSUE=Spleen;
MEDLINE=99285539; Pubmed=9620874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 AYGLSDQLAQAISDHYPVEVMLK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 AYDLSEERALDVSDHFPVEFKLQ 287
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Biochemistry 37;10134-10143(1998).
                                                                                                                                                          35760 MW;
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                                                                                                                                                                                                                       Best Local Similarity 46.4%
Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- PTM. SERIES TO BE SYNTHERIZEDS AS AN IMACHIVE PRECURSOR PROTEIN AND CONTERTED INTO AM ACTIVE MATURE BYZNYE BY REMOVAL OF THE N. TZEMINIAL PRECURSOR PRETUIDE DIRING ACPORTS REMOVAL OF THE N. STEMICHARDONS: ACTIVE OVER A BROAD HE RAMES (OFTINUT HF 7-8).
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ESSENTIAL FOR ENZYMATIC ACTIVITY
(BY SIMILARITY).
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PROSITE, PS00918 MASE I 2; 1.
PAYCOLASE; ENODALG MASE I NUCLEAS.
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BIPARTITE NUCLEAR LOCALIZATION SIGNAL
(POTENTIAL).
                                                                                             Shiokawa D., Ohyama H., Yamada T., Tanuma S.-I.; Purification and properties of DNase gamma from apoptotic rat
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45.6%; Pred. No. 3e-48;
tive 47; Mismatches 92; Indels
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PARTIAL SEQUENCE, AND CHARACTERIZATION.
MEDLINE-97439708; PubMed=9307016;
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InterPro: IRR005135; Exc_endo_phos.
Pfam, PR03372; Exc endo_phos.
PRINTS; RR00130; DNasEI.
PRODOM; PD005409; DNase_I. N; 1.
SNART; SNART; SNO0476; DNase_I. N; 1.
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EMBL; U75689; AAC40134.1; -.
HSSP; P00639; 3DNI.
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160 160 B
310 AA, 35708 MW;
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179 SQWSSIRLWTSPTFQWLIPDSADTTA-TPTHCAYDRIVVAGMLLRGAVVPDSALPFNPQA 237
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HSSP, P00639, 3DNI.
Genew, HGNC:2959, DNASELL3.
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                          119 FSRFTEVREFALVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRP 178
                                                                                                                   145 OAPETAAKDEVIVELHTTPETSVKEIDELADVYTDVRRRWKAENFIFWGDENAGCSYVPK 204
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yanka cloning of human DName gamma: chromosomal localization of its
gene and enzymatic properties of recombinant protein.";

properties 3:69-95(1989).
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Mammalia, Butheria, Primates, Catarthini, Hominidae, Homo.
17_TaxLp=5666,
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Schräfiguez A.M., Rodin D., Nomura H., Moxton C.C., Weremowicz S.,
Schnätder M.C.;
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Baron W.F., Pan C.Q., Spencer S.A., Ryan A.M., Lazarus R.A.,
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A Backelguez A.C., Grimono d.J., Schwartz J., Where R.M.,
A Backelgued Y.S. M. Krzywinski, M.T., Skalsku U., Smailus D.E.,
Schwerch A., Schwin G. E., Jones S.J.H., Marter M.A.;
A Charaction and initial analysis of more than 15,000 full-length
Twenserrich and paragements. A 91;6899-18901(2002).
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Conservative 51; Mismatches 89; Indels
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BAB9F1A0341E6048 CRC64;
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EMBL, AR047354.7; -.
EMBL, U15744; AAC2362.1; -.
EMBL, BC015831; AAH18831.1; -.
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155 155 BY
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305 AA, 35504 MW;
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"Generation and initial analysis of more than 15,000 full-length
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HSSP; P00639; 2DNJ.
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SEQUENCE FROM N.A.

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SEQUENCE STATE FELGROID E.A. GEONNE L.R., DETCE J.G., D. G.

STRIAMED STATE FELGROID E.A. GEONNE C.M., SCHILLET G.D.,

A. ALTGENIE R.F. COLLINE S. MARDEL. E. SCHWINGER, M.M. SCHILLE G.M., SCHILLE G.M., SCHILLE G.M., SCHILLE R.F.

A. ALTGENIE R.F. COTCHEN H. WOOTE T., WAN S.I., WEND J., WEND L. M. STRIJECOM, S. GOACE M.B., BORNIGH G.M., BORDING J., MERGER T. B., STRIJECOM, SOACE M.B., TORGEN T. W., SCHOET T. E., BERNES S., MCHORLIBRO N.A., PERCER G.J., Abramon R.D., MILLIBY S.J.,

BORNES S.S., MCHORLIBRO N.A., PERCER G.J., Abramon R.D., MILLIBY S.J.,

M. MCHARGE S., WORLEW R.C., MALE S., GERCIE A.M., GSULLE, M.M.,

M. MILLIAME D.K., MARTYD JM., SOCHETER E.J., LM. X., GSIDER R.A.,

M. MILLIAME M. MAGAN A., WOULG A.C., SCHWCHONFO Y., BONKEA'G.G.

M. BARRES S.W., TOUCHAM I.W., OFFICE E.D., DECKNIESE S. BRANCK A.

MILLIAME S. A.C., GERMOND J., SCHWULT J., WESTER R.M.,

MILLIAME S. A.C., GELWOOD J., SCHWULT J., WESTER R.M.,

MILLIAME S. A.C., SCHWUND J.W., OFFICE S. M.S., SHANDA A., MCANNAN A.
200 KAWKNIRLRIDDRFVWLIGDGEDTIVKKSINCAXDRIVLRGGEIVSSVVDKSNSVFDFQK 259
                                                                                                                                                                                                                                                                                                                      01-FEB-1956 (Reb. 33, Lasts sequence update)
11-EER-2000 (Reb. 142, Lasts annotation update)
11-EER-2000 (Reb. 142, Lasts anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96194910, PubMed=8654957,
Pergolizzi R., Appierto V., Bosetti A., Debellis G.L., Rovida E., .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Long-range sequence analysis in Xq28; thirteen known and six candidate genes in 219.4 kb of high GC DNA between the RCP/GCP and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen E.Y., Zollo M., Mazzarella R.A., Ciccodicola A., Chen C.-N., Zuo L., Heiner C., Burough F.W., Ripetto M., Schlessinger D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96081217; PubMed=8541839; Parksh J.E., Ciccodicola A., Wehnert M., Cox G.F., Chen E., Nelson D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COY J.F.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A muscle-specific DNase I-like gene in human Xq28.";
Hum. Mol. Genet. 4:1557-1564(1995).
                                                                                                                                                                                                                                                                           PRT; 302 AA.
                                                                                 238 AYGLSDQLAQAISDHYPVEVMLK 260
                                                                                                                260 AYKLTEERALDVSDHPPVEFKLQ 282
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MEDLINE=96311563; Pubmed=8733135;
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P49184;
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9, Gaps
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BY SHFLLARITY

L-NINKED (LGLAGC, .) (FOTENTIAL).

L-> I (IN REF. 2, AABOO496).

G-> G IN REF. 2, AABOO496).

G-> KIN REF. 2, AABOO496).

G-> KIN REF. 2, AABOO496).

MP. DIQUESHSYDINJYJYY (RC64).
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MUSCLE-SPECIFIC DNASE 1-LIKE.
ESSENTIAL FOR ENZYMATIC ACTIVITY
(BY SIMILARITY).
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ILLERFORD, IRROGOLSES; Dasael.
ILLERFORD, IRROGOLSES; Exc. endc. pincs.
PRINTS; PROGOLSO; DASAEL.
PRINTS; PROGOLSO; DASAEL.
SALAT; PROGOLSO; DASAEL.
SALAT; PROGOLSO; DASAEL.
PROGOTTS; PROGOLSO; DASAELC; I.
PROGOTTS; PROGOLSO; DANASELC; I.
PROGOTTS; PROGOLSO; PROGOTTS; PROGO
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EMBL; L40823; AAB00496.1;
EMBL; U44440; AAA92647.2;
EMBL; U00646; AAB17022.1;
EMBL; EC001551; AAH0156.11;
EMBL; EC020924; AAH38092.1;
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-i- CAPPING THE STATUTT: N mucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIATINE 311400, PURAGAL-18565A.

Sate T., Meroyean H., Xahutani T., Ridaka S., Kiguchi T., Nagara R., Sate T., Meroyeani P., Nishisunchi M., Anther Complete nuclectide sequence of cucumber green mottle mosato "Xiria (Sig Estalin) genomic RNA".

3. Gen. Virbl. 72.1487-1495 (1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ggaki M., Tomiyama M., Kakutani T., Hidaka S., Kiguchi T., Nagata R.,
Ggor T., Mocyoshi F., Mishiguchi M.
Submitted (EB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SABIC T., Imal Y., Weshi T., Okada Y.,

"Intervise homologies of the 30% procesins of tobamoviruses.";

"Intervise homologies of the 30% procesins of tobamoviruses.";

-- PROGRAMS SEGGI 988)

-- ROWGINS THE LOWGER PROTEIN IS A RNA POLYWERASE ACTIVE IN VIRAL.
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CHAIN 1 1646 RNA-DIRECTED RNA POLYMERASE.
CHAIN 1 1144 METHYLTRANSFERASE/RNA HELICASE.
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InterPro; IRR007095; RNA_Dol_DS_PS-
INTERPO; IRR007094; RNA_DOL_PSOTIT-
INTERPO; IRR007094; NA_DOL_PSOTIT-
INTERPO; IRR00706; VITAL_NALCASSE.
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Pfam; PF01443; Viral helicasel; 1.
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ID RRPO CGMVS
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1373 FKXLITKFLSMVDSSKFFFY------TRKKPEDLQEFFSDLSGHSDYEILELDVSK 1422
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                                                                                                                                                                92 ------VDS---YYYDDGCEPCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAP 137
                                                                                                                                                                                                                                                            138 GDAVAELDALYDVYLDVQEKWGLEDVM-----LMGDFNAGCS----YVRPSQWS 182
                                                                                                                                                                                                                                                                                                                                                                183 SIRLWISPIP-----CWLIPDSADITATPIHCAYDRIVVAGMLLRGAVVPD----SALP 232
                                                                    46 TAVGKLIDNINODAP--DTY-HYVVSEPLGR-----KSYKERYLFVYRPDQVSA---- 91
1 Similarity 22.9%; Pred. No. 0.44; 56; Conservative 37; Mismatches 81; Indels 71; Gaps
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	* Query Match	82.7	80.4	80.2	77.8	77.5	58.8	58.6	55.5	54.7	50.8	49.6	49.1	48.8	46.0	45.9	45.8
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w	44.9	43.5	34.9	11.8	11.6	9.4	7.4	7.4	7.4	6.9	6.9	8.9	6.7	6.9	6.7	6.7	6.3	6.7	6.7	9.9	6.5	6.5	6.5	6.5	6.4	6.4	6.4	6.4	6.4
<b>ままととららないにももともともできないないないできます。まままままままままましょうものしょころもももしょうないににもないのものものものものものものものものものものものものものものものものものもの</b>	613.5	595	477	161	158.5	128	100.5	100.5	100.5	94.5	94	93	91.5	91.5	91	91	91	16	16	90	89.5	88	88.5	88.5	88	87	87	87	87
	11	18	13	20	22	55	23	24	52	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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Ouery Match
Best Local Similarity 81.7% Pred. No. 5.18-103; DB 11, Length 284;
Matches 2.3; Conservative 23, Mismatches 24; Indels 0; Gaps
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                                                                                                                                                     01-DEC-2001 (TrEMBirel. 19, Created)
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8imilar to deoxyribonuclease I.
PRT,
PRELIMINARY;
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Mus musculus (Mouse)
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Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

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PRELIMINARY;
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TISSUE=Salivary gland;
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121 RFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPSQ 180
                                                                                                                            143 PYTEVQEFAIVPLHAAPTEAVSEIDALYDVYLDV#QK#GLEDIMF#GDFNAGCSYVTSSQ 202
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Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TAXID99823,
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01-DEC-2001 (FrEMBirel, 19, Last sequence update)
01-MAR-2003 (FrEMBirel, 23, Last annotation update)
Decogribonuclease 1.
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193 QWLIPDSADTTATPTHCAYDRIVVAGWLLRGAVVPDSALPFNFQAAYGLSDQLAQAISDH 252 Z83 QWLIPDSADTTATPTHCAYDRIVVAGALLQAAVVBNSAVPPFDFQARSKQLAEAISDH 322 QWLIPDSADTTYTSHCAYDRIVVAGALLQAAVVBNSAVPPFDFQDEYRLSKQLAEAISDH 322
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80.2%; Scoze 1097; DB 11; Length 332;
Best Local Similarity 69.2%; Pred. no. 1.4e-92

Matches 213; Conservative 23; Mismatchee 24; Indels 48; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chozdata, Craniata, Vertebrata, Buteleostomi;
Mammaliat, Entheria, Rodentia, Sciurognathi, Muridae, Muthne; Mus
KGELTATO-10950;
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
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01-000-2002 (TEMBLER). 22, Last sequence update)
101-004-2003 (TEMBLER). 23, Last amnocation update)
100-048-2003 (TEMBLER). 22, Last amnocation update)
100-048-2003 (TEMBLER). 22, Last amnocation update)
100-048-2003 (TEMBLER). 23, Last amnocation update)
100-048-2003 (TEMBLER). 24, Last amnocation update)
100-048-2003 (TEMBLER). 24, Last amnocation update)
100-048-2003 (TEMBLER). 25, Last amn
                                                                                                            01-007-12002 (TrEMBER-21 22, Created)
01-007-2002 (TrEMBER-21 22, Last sequence update)
03-MR-2003 (TrEMBER-21 22, Last amnoration update)
03-MR-2003 (TrEMFER-21 22, Last amnoration update)
MNH muschilds (Wouse)
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PRT; 332 AA.
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InterPro, 189001452, Danse, 1.

InterPro, 189001452, Danse, 1.

Pean, Projatz, Exc. endo. phos.

Pean, Projatz, Exc. endo. phos.

Percolom, Projatz, Exc. endo. phos.

Prochom, Projatz, Projatz, 1.

PROSTER, PROJAS, PARSE, 1.1.

SEQUENCE 312 AA, 37759 WM, 1A08890
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Mammaliai Buthoriai, Octartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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Best Local Similarity 77.6%; Prof. No. 2e-96, DB 6; Length 282;
Natches 201; Conservative 39; Mismetches 29; Indels (
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                    De Maria A.B., Arruti C.;
Provine DN881 gene for deoxyribonuclease I.";
submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AFS28509; AAM91248.1; -
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282 AA; 31331 MW; 4385BB10C00700E2 CRC64;
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01-MAR-2001 (TERBELFE) 25, Late sequence update)
01-MAR-2003 (TERBELFE) 23, Late sequence update)
01-MAR-2003 (TERBELFE) 23, Late annotation update)
Bos taurus (Bovino).
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190 MSSIRLWISPIPOWLIPDSADTIATSHOANGAILRGAVAVPDGALPERFOAAVS
191 MSSIRLWISSIPOMLIPDSADTIATSHOANGAYRAIVAGSLAGSSVPSPEDQAAVS
252 MSSIRLWISSIPOMLIPDSADTIATSHOANGAYRAIVAGSLAGSSVPSPEDQAAVS
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                                                                                                                                                                                                                                                                                                     13 LKIAAFNIRTFGETKASNATLASYIVRIVRRYDIVLIQEVRDSHLVAVGKLLDYLNQDDP 72
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Submitted (Juli 2000) to the ENBL/GenBank/DDBJ databases.
ENBL, ABOSTAN, BARSOSG.1;
ENBL, ABOSTAN, ENBROSG.1;
ENBL, ABOSTAN, ENBROSG.1;
ENBL, ABOSTAN, ENBROSG.1;
ENBREADO, TREADOLIST, ENBROSG.1;
ELABOSTAN, ENBROSG.1;
ENBREADO, TREADOLIST, ENBROSG.1;
ENBREADO, TREADOLIST, ENBROSG.1
ENBREADON, TOBOSTO, ENBREADOLIST, ENBROSG.1
ENBREADON, TOBOSTO, ENBREADOLIST, ENBREADON, TOBOSTO, ENBR
                                                                                                                                0; Gaps
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Query Match 77.5%; Score 1060; DB 6; Length 272; Best Local Similarity 77.6%; Pred, No. 4.78-69; Maches 201; Conservative 28; Mismatches 30; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 58.8; Score 804; DB 13; Length 28; Secre 804; DB 13; Length 28; Sect No. 9.44-7; Matches 152; Observative 43; Manatches 65; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
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01-DEC-2001 (TrEMBIrel. 19, Last sequence update)
01-MR-2003 (TrEMBIrel. 29, Last annocation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 LSDQLAQAISDHYPVEVML 259
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Takeshita H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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61 DYYHYVVSEPLGRKGYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120
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142 PTGLEBEVYUVEHARBACAAEINALDVYTOVINKAEINXIFFWGDRADGSYVAEQ 201
142 PTGLEBEVYUVEHARBACAAEINALDVYTOVINKAEINXIFFWGDRADGSYVAEQ 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 YPYSFLSSIPLGRNSYKEQYVFIYRSDIVSVLESYYYDDGCESCGTDIPSREPFIVKFSS 141
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                                                                                                                               Gallus gallus (Chicken).
Bukaryota, Metazoa, Chordata, Craniata; Vertebrata; Buteleostomi;
Archosauxia, Ases, Neognethae; Galliformes; Phasianidae, Phasianinee;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
55.5t; Score 759; DB 13; Length 283;
Best Lost Similarity 58.1%; Pred. No. 2.3e-6.7
Matches 15; Conservative 3; Mismatches 75; Indels 0; Gaps
                                                                                                                                                                                                                                                                              SEQUENCE PROM NA.
MAKAGEMEN Y. 784ed-10605824;
MAKAGEMEN Y. 784ed-10605824;
MAKAGEMEN Y. 784ed-17., 784ed-16605824;
MAKAGEMEN Y. 784ed-17., 784ed-17., 784ed-17., 784ed-17., 784ed-17., 784ed-17., 784ed-17., 784ed-17., 784ed-18., 784ed-18.
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Actinopteryota; Mesotas; Chordata; Craniata; Vertebrata; Bureleoscomi;
Actinopterygli; Meopterygli; Teleostei; Ostariophysi; Opprinifozmes;
Yorlinden-962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mogi K.;
"Carp DMase I.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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PRODOM: PD003406 DYSee 1; 1.
PROCENTS: SNOO476; DMSsed.7; 1.
PROCETTS: PS00419; DMSsed.7; 1.
PROCETTS: PS00419; DANSE 1.2; 1.
SEGUENCE: A33 AA, 3.1455 WH; ESES2596E33DFC600 CRC64;
                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Decayribonuclease 1.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro: IPR001582; DNase I.
Interpro; IPR005135; Exc endo phos.
Pfam; PF03372; Exc endo phos; 1.
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Q8JIP7;
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201 WSSIRLSKENDPHILIPINATOTATWOVANDRIVAVESKIRRSKIRARAKVUBFORTIK 260
202 WPSIRLESKENDPHILIPINATOTATWOVANDRIVAVARKIRRSKIRARAKVUBFORTIK 260
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181 WSSIRLWISPTRQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPPNFQAAYG 240
                                                                                                                                                                                                        201 WPSIRLRSSKDFQWLIPDTADTTVTNTICAYDRIVAVGSKLRESILPATAKVDNFQKTLK 260
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SMEL, NSOSYOU, PARSESSEL1, F.
ILREFPO, IRROSLESSEL, IL.
ILREFPO, IRROSLESSEL, EXC. and D. DRG.
REAM, PROSLESSEL, INSERE, I. I.
PROSLESSE, PROSLESSEL, I.
PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSLESSEL, PROSL
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Agkistrodoń halys pallas (Chinese water mocassin) (Gloydius halys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buceleostomi;
Leptdosauta; Squamta; Scleroglossa; Serpentes; Colubroidea;
Viperidas; Croalinae; Gloydius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 58.6%; Score 801; DB 13; Length 282; Sest Local Similarity 58.5%; Pred. Mo. 1.7e-70. Matches 152; Conservative 43; Manatches 65; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAR-2002 ("PEMBLrel. 20, Created)
01-WAR-2002 (TEMBLrel. 20, Last sequence update)
01-WAR-2003 (TEMBLrel. 23, hast annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 282 AA.
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Q9PTY8
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QSUWB6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 IRIGAENVQSFGDNKVSDPDCGSVIAQILAGYDIALVQEVRDPDLSAVSLLMEQINRVSK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 50.8%; Score 694.5; DB 11; Length 278; Best Local Similarity 53.5%; Pred. No. 5.8-60; Makches 139; Conservative 36; Misumatches 80; Indels 5;
BMEL, AKO03619; BA8228993.1; -.
BMEL, AKO03619; BA8228993.1; -.
BMESP; PROSO37 ZDMJ
THEATPO; TRYO01589; DARSeg. 1.
THEATPO; TRYO01589; DARSeg. 1.
THEATPO; TRYO0159; DARSeg. 1.
REMAY FROOT30; DARSeg. 1.
REMAYS; RROOT30; DARSEG. 1.
SWART; SROOT46; DARSEG. 1.
SWART; 
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01-JTW-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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Q9D645;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 SNTAVQQKFALVPQHTSPEVAVTEIDALHDVVLDTRQRLNTNNIMLLGDFNAGGSYVSNS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 DASKIRLATDQSYTWLIPDSADTTVTHTWCPYDRIVATSDWRKG-VSAGSAQVPDFWQAH 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 PYEYQYIVSEPLGRSTYKERYLFIYRRQAVSVANSFQYDDGCESCGTDTFRREPFVVMFS 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 PDTYHYVVSEPLGRKSYKERYLPVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 SRFTEVREFALVPLHAAPGDAVAELDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LAIAARNIQTRGETKARNATUSYIVQILSRYDIALVQRYRDSHLTANGKLLDNIA-QDA 59
20 LIJQARIKSRÇOSKASNATLOLITRVHRYDIVLQRYRDSDLTANKLAMSVNGSS 79
20 LIJQARIKSRÇOSKASNATLOLITRVHRYDIVLQRYRDSDLTANKLAMSVNGSS 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Gaps
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Mammalia, Butherla, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.7%; Score 748; DB 13; Length 279; 55.4%; Pred. No. 2.7e-65; ive 40; Mismatches 74; Indels 2
                  | InterProj (PRODISE) | InterProj (PROSISE) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TERMELrel. 17, Created)
01-JUN-2001 (TERMELrel. 17, Last sequence update)
01-JUN-2002 (TERMELrel. 21, Last annocation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 144; Conservative
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121 RFTEVREFALVPLHAAPGDAVAEIDALVDVYLDVQEKWGLEDVMLAKGDFRAGCSYVRPSQ 180
137 PSCATFELVLFELHAAPGAVAEIDALVDVILDVICKWNTDMLFLCFFRAGCKVVAHD 196
137 PSCATFELVLFFLHAAPGAVEIDALVDVILDVICKOVICTOMLFLCFFRAGCKVAHD 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 WSSIRLWISPIRGWLIDDSADTIATPIHCAYDRIVVAGWLLRGAVVPDSALPFNFGANG 240
197 WSIRLNSSEVRWILDDSAHITVGNSDAVDRIVVSGAHRRISKPSAFWRRQEED 256
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Takeshita H. Yasuda T. Jida R., Nakajima T., Mori S., Mogi K.,
Takeshita H. Yasuda T. Jida R., Nakajima T., Mori S., Mogi K.,
Takeshita H. Yasuda T. Jida R., Nakajima T., Mori S., Mogi K.,
"Amphikain Dakasa I see characterized by a C-terminal end with a
into a Cas-binding street, and by the insertion of a serine residue
into a Cas-binding street,
EMEL, Margh 15, 1871-480 (2001).
EMEL, Margh 15, Margh 1.
InterPro, TRR001312 S. Koc endo phos.
InterPro, TRR001312 S. Gondo phos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Gaps
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Rana catesbeiana (Bull £rog).
Bubaryota; Metacola, Chanata, Craniata; Vertebrata; Exteleostomi;
Bubaryota; Metacola, Anura, Kaosatrachia, Ranoidea; Rana.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 19, 64; Score 679.5; DB 11, Length 278, Best Local Similarity 52.78; Pred. No. 198-59, Maches 187; Conservative 36; Mismatches 62; Indels 5;
                                                                                                                             PROSITE; PS00524; SOMATOMEDIN B; 1.
SEQUENCE 353 AA; 39192 MW; P7AFC30AB05E607A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Deoxyribonuclease I.
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Pfam; PF01033; Somatomedin_B; 1.
PRINTS; PR00130; DNASEI.
Nature 409:685-690(2001).
EMBL; AKO14633; BAR29476:1; -.
EMSF; PO0639; 2DNJ.
MGS; MGI:1913955; 4733401H14Rik.
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SMART; SM00476; DNaseIC; 1.
SMART; SM00201; SO; 1.
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61 DTYHYVVSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPALVRFFS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 LSYNLLISDHIGRSAYREKYVVVYREDILKPTEWFHYDDGCENCGTDVFMREPFVARFSS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 LTTEVKDFALAVVHTSPDYAVREVDALFDVWEDAKQRLLMEDIFILGDYNAGCSYVKSAH 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 WSSIRLWTSPTFQWLIPDSADTT-ATPTHCAYDRIVVAGWLLRGAVVPDSALPFNFQAAY 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DIYHYVVSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120
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                                                                                                                                                                                                                    1 LKIAAFNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAP 60
                                                                                                                                                                                                                                                                                                          20 LKIAGFNIERFSATKVDDPVVLNRLIQILRRYELIAVQSVMKDDTAIIKLVRELNKATG 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bufo japonicus (Japanese toad).
Bukaryota, Metaroa, Chordata, Caniata, Vertebrata, Buteleostomi;
Amphiba, Bartachia, Anura, Neobarrachia, Bufonoidea, Bufonidae, Bufo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scotters and the control of the cont
                                                                                                              1; Gaps
Ouery Match
Best Local Similarity 49.1%; Pred, No. 138-57, 138-57, Matches 126; Conservative '59, Mismatches 75; Indels 1; Matches 126; Conservative '59, Mismatches 75; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery March 48.8%; Score 666.5; DB 13; Length 353; Sept Local Similarity 46.4%; Prefel No. 4.1e-57; Marches 121; Conservative 61; Mismatches 77; Indels 1; Marches 121; Conservative 61; Mismatches 78; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 353 AA; 39295 MW; 761BBE288724AB5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMELrel. 19, Created)
01-DEC-2001 (TrEMELrel. 19, Last sequence update)
01-DEC-2001 (TrEMELrel. 3; Last annotation update)
01-MAR-2003 (TrEMELREL. 3; Last annotation update)
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PRINTS, PROUJO, DAMAGET.

SWART, SNOO476; DMaged_i, 1.

SWART; SNOO476; DMaged_i, 1.

SWART; SNOO476; DMaged_i, 1.

PROSITE, PROUZO1, SO, 1.

183

PROSITE, PROUZO1, SO, 1.

183

PROSITE, PROUZO1, SO, 1.

183

PROFITE, PROUZO1, SO, 1.

PROFITE, PROFITE, PROUZO1, SO, 1.

PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROFITE, PROF
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Search completed: November 21, 2003, 13:56:34
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                                         181 WSSIRLWTSPTFQWLIPDSADTT-ATPTHCAYDRIUVAGWLLRGAVVPDSALPFNBQAAY 239
                                                                                                                                                                                               200 WPNIRLROESSLOWLIGDIEDSTWSTNIHCPYDRLVVGGARFODTVIPGTAKAFNYHVAY 259
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WEDINE-10541222; PubMed-11097135;
Hosomi O., Yasuda T., Takeshira H., Nakajima T., Nakashima Y.,
Nori S., Woga K., Handska I., Klaji K.,
Nori S., Woga K., Handska I., Klaji K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus lacvis (African clawed frog).
Bukaryota; Metazoa, Chordara; Cranidar; Vertebrata; Buteleostoni;
Amphibia; Barzachia, Amura; Mesobarzachia; Pipoidea; Pipidee;
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01-MRR-2001 (TrEMBLrel. 16, Last Sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
peoxythogonuclease I.
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INTERFOR PRO01582; DANSE I
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INTERFOR PRO01592; DANSE I
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INTERFOR PRO01590; DANSE I
INTERFOR PRO015
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261 LTYEMAKAVSDHYPVEVEL 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae, Xenopus.
NCBI_TaxID=8355;
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59 APDIYHYVVSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRF 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LKIAAFNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLN--QD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Gaps
                                                                                                                                                                                                                                                                                                          Decyyriboniclease gamma.
Xenogua laevis (African clawed frog).
Nakryota, Mecazoa; Chordata, Cranata, Vertebrata, Bureleostomi;
Amphibia; Batrachia; Amura; Mesobatrachia; Pipoldea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13; Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sinciera Di 'Tranma S.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 45.9%; Score 628; DB 13; Length 29
Best Local Similarity 47.9%; Pred. No. 2e-53;
Matches 126; Conservative 47; Mismatches 86; Indels
                                                             Opyrod,
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
295 AA.
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE PROM N.A.
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## GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

Copyright (c) 1993 - 2003 Compugen : OM protein - protein search, using sw model Run on: November 21, 2003, 13:46:51 , Search time 11 Seconds Withbort alignments of S23:849 Million cell updates/sec

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 328717 sege, 42310858 residues

Searched: 328717 seqs, 42310858 residues Total number of hits satisfying chosen parameters: 328717

Minimum DB seg length: 0 Maximum DB seg length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : Issued Patents A.1.\*a./SA.COMB.pep;\*
21. /GRTZ 6/prodats/1/18.6/ZOMB.pep;\*
22. /GRTZ 6/prodats/1/18.6/ZOMB.pep;\*
31. /GRTZ 6/prodats/1/18.6/ZOMB.pep;\*
51. /GRTZ 6/prodats/1/18.6/ZOMB.pep;\*
51. /GRTZ 6/prodats/1/18.6/ZOMB.pep;\*
61. /GRTZ 6/prodats/1/18.6/ZOMB.pep;\*
62. /GRTZ 6/prodats/1/18.6/ZOMB.pep;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is detrived by analysis of the total score distribution.

## SUMMARIES

		Appli	, Appl	Appli	Appli	Appl,	Appli	Appli	Appli	Appli	Appli	App12	Appl	, Appl	Appli	Appli	Appli	Appli	, Appl	, Appl	6, Appl	Appli	Appli	, Appl	Appli	Appli	Appli	Appli
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		JS-08-663-831-	US-08-663-831-10	US-09-796-774-	08-663-831-	US-08-663-831-1	-10-074-509-4	US-07-895-300A-	US-09-638-112-1	PCT-US93-05136	JS-08-663-831-	US-08-663-831-	US-08-663-831-	JS-08-663-831-1	JS-08-663-831-4	US-08-458-367-	US-08-663-831-	JS-08-663-831-	US-08-663-831-	US-08-663-831-	-08-663-831-	JS-08-663-831-8	-08-663-831-7	JS-08-663-831-	JS-08-640-765A	-09-073-613-	US-10-074-509-	10-074-509-
1	8	US-08	US-08	US-09	US-08	US-08	US-10	US-07-	OS-09	PCT-US	US-08-	0S-08	-80-SD	US-08	-80-SD	US-08-	-80-SD	0S-08	-80-SD	US-08	-80-SD	US-08-	US-08	ns-08	-80-SD	US-09	US-10	US-10
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	Length	260	260	260	260	260	260	346	346	346	260	260	260	260	260	346	260	260	260	260	260	260	260	260	310	310	285	305
Query	Match	100.0	99.8	99.66	9.66	99.66	99.6	9.66	99.6	99.6	99.3	99.3	99.3	99.3	99.3	99.3	99.2	99.2	99.3	99.2	99.2	0.66		98.9	43.3	43.3	43.2	43.2
,	Score	1367	1364	1362	1362	1362	1362	1362	1362	1362	1358	1358	1358	1358	1357	1357	1356	1356	1356	1356	1356	1354	1353	1352	592	592	291	591
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Query Watch 100.0%; Score 1367; DB 4; Length 260; Bset Local Similarity 100.0%; Pred. No. 3.6e-152. Metches 260; Conservative 0; Mismatches 0; Indels 0;

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	1 US-07-895-300A-14	14	Appl

## ALIGNMENTS

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61 DYYHYVVSEPLGRNSYKERYLFVYRPDQVSAVDSYYDDGCEPCGNDTFNRSPAIVRFFS 120
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181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAYG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IKIARAFNIQTFGETKMSNATLVSYIVQILSRXDIALVGEVRDSHLTAVGKLLDNLNQDAP 60
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TITLE OF INVENTION: HUMAN DNASE I VARIANTS NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARTICULAR WARREN (04/92998)
FIREMONT WARREN 1997-1997
FILEMONT WHEREN 10/07-1995
FILEMON WARREN 10/07-1995
FILEMON WARREN 10/07-1995
FILEMONT 14-MPA-1995
FILEMONT WARREN 1995
FILEMONT WARREN 1995
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NAME: Johnson, Sean A:
REGISTRATION NUMBER: 35, 910
REFERRINGE/DOCKET NUMBER: P9925F1C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
SYREET: 1 DNA May
CITY: South San Francisco
SYATE: California
COUNTRY: USA
                                                                                                           241 LSDQLAQAISDHYPVBVMLK 260
                                                                                                                                                 241 LSDQLAQAISDHYPVEVMLK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lazarus, Robert A.
Shak, Steven
                                                                                                                                                                                                                                                                                                                                                                                       US-09-796-774-1

, Sequence 1, Application US/09796774

; Patent No. 6348343

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 260 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 650/225-3562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Generatech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.6%
Matches 259; Conservative
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121 RFTSVREAT AVLLIAAGDAVAEIDALYDVLDVQEKWGLEDVALMGDFBAGGSYVRPSQ 180
121 RFTSVREAT AVLLIAAGDAVAEIDALYDVLDVQEKWGLEDVALMGDFBAGGSYVRPSQ 180
                                                                                                                                                                                                                                                                                                                                                181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAYG 240
                                                                                                           121 RFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPSQ 180
                                                                                                                                                                181 WSSIRLWISPIFQWLIPDSADITATPIHCAYDRIVVAGMLIRGAVVPDSALPFNFQAAYG 240
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       61 DTYHYVVSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120
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Bost Local Similarity 99.6%; Pred. No. 8e-121;
Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICARY: Tan Clark Own THERACTIVE VARIANTS THIS OF SECURITY AND CLARK OWN THIS OF SECURITY SHOWS THE SEATON OWNERS IN THIS OF INVESTIGATION THORSES IN CORRESSON GENERAL ADDRESSES. Generate Cell Inc. Security 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,831
FILING DATE: 14-Jun-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 LSDQLAQAISDHYPVEVMLK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 LSDQLAQAISDHYPVEVMLK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/08663831
Patent No. 6391607
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DUS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Johnston, Sean A.
REGISTRATION NUMBER: 35,910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3562
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 10:
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LENGTH: 260 amino acids
TYPE: Amino Acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
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61 DTYHYWYSDLAGANSYKERYLFVYRPDQVSAVDSYYDDGCEFCGNDFRREAITRFF 120
61 DTYHYWYSDCANSYKERYLFVYRPDQVSAVDSYYDDGCEFCGNDFRREAITRFFF 120
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99.6$; Score 1362; DB 4; Length 260;

gest Local Similarity 99.6$; Pred. No. 1.4e-150.

Matches 259; Conservative 0; Mismatches 1; Indels (
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APPLICANT: PARACLASK DANACLAR OF APPLICANT: PARACLASK DANACLAR OF APPLICANT: PARACLASK DANACLASK DANACLA
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MEDIUM YTER: 3.5 inch, 1.44 Mb floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,831
FILING DATE: 14-7um 1996
CLASSIFICATION: 435
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NAME JOHNSON, SEAN A, 1910
REGISTRATION NUMBER: 9, 29, 10
REFERENCE/COCKET NUMBER: P. 19, 20
RELEPHORE, 115/235-3861
TELEPHORE, 115/235-3861
TELEPHORE, 115/235-3861
TELEPHORE, 115/235-3861
TELEPHORE GARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                          US-08-663-831-1
; Sequence 1, Application US/08663831
; Patent No. 6391607
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Amino Acid
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61 DTYHYVVSBPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120
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APPEDOMET PARENCETUR VARIANTS
TITLE OF INVENTION: HUMAN DNASE I HYPERACTIVE VARIANTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                      ; Sequence 14, Application US/08653831; Parent No. 6391607; GENERAL INFORMATION:
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TYPE: Amino Acid
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APPLICANT: Baker, Kevin P.

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121 RFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLWGDFNAGCSYVRPSQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REMARKE FORM:

MEDITAM TYPES: 5.25 inch, 560 Kb floppy disk
COMPUTER: 18M PC compatible
ODPATING SYSTEM: PC-005/MS-DOS
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GENERAL INFORMATION:
AFPLICANT: Frent, John
AFPLICANT: Staven J.
AFPLICANT: SIANCANAT, Mary B.
TITLE OF INVENTION: PURITIED FORMS OF DNase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
APPLICANT: Sliwkowski, Mary B.
11TLE DE INVENTION: PURIFIED FORMS OF DNASE
UNMERS OF SECUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/07/895,300A
                                                                                                                                                                                             ADDRESSEE: Genentech, Inc.
STREEF: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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REGISTRATION NUMBER: 27,043
REFERENCE/DOCKET NUMBER: 747
TELECOMMUNICATION: 1NFORMATION: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415/952-9881
TELEX: 910/37-7168
INPORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 346 amino acids
TYPE: AMINO, ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POPOLOGY: linear
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CORPUTER: 180 FC convariable
CORRATION SYSTEM: FO.005/MS-DOS
SOFTWARE: Mither in (Generach)
CURRATION MARKER: 105/10/074, 509
FILIND DAYS: 11-F6-2002
CLASSIFICATION NATE: 11-F6-2002
CLASSIFICATION NATE: 11-F6-2002
FILIND DAYS: 11-F6-2003
FILIND DAYS: 11-F6-2003
FILIND DAYS: 10-F6-1907
FILING DAYS: 11-F6-2003
FILING DAYS: 10-F6-1907
FILING DAYS: 11-F6-2003
FILIN
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-074-509-4
                                             TITES OF INVENTIONS INTO NAME OF CORRESPONDING ADDRESS.

STREET IN MAY MAY CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE OF CONTINUE CONTINUE CONTINUE CONTINUE CONTINUE OF CONTINUE CONTIN
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INFORMATION FOR SEC IN NO: 4: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: TYPE: Manino Acide
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Facent No. 2278923
GENERAL INFORMATION:
APPLICANT: Frenz, John
APPLICANT: Shire, Steven J.
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               Baron, Will F.
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US-07-895-300A-1
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0; Gaps

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61 DIYHYVVSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ondery Match 99.6%; Score 1362; DB 5; Length 346; Best Local Similarity 99.6%; Pred. No. 2.18-150. Metches 259; Conservative 0; Mismatches 1; Indels (Matches 1); Conservative 0; Mismatches 1; Indels (Matches 1); Conservative 0; Mismatches 1); Conservative 0; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7. Application US/08663811
GREAT INFORMATION:
APPLICANT: Learners Robert A.
APPLICANT: Learners Robert A.
APPLICANT: Part, Clark Qun
TITLE OF TRYBETORY: HUMN DWASE I HYPERACTIVE VARIANTS
WOMBER OF SEQUENCES: 17
CORRESPONDER ADDRESS:
ADDRESSER: Generorech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER RELDABLE FORM:
HEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER: 18H PC compacible
OPERATING SYSTER: PC-D02/NS-D0S
OPERATING SYSTER: PC-D02/NS-D0S
OPERATING SYSTER: PC-D02/NS-D0S
OPERATING SYSTER: PC-D02/NS-D0S
PC-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/NS-D02/
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US93-05136-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DTYHYVVSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 RFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 WSSIRLWISPIFFOWLIPDSADTIATFIHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAYG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLIRGAVVPDSALPFNFQAAYG 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 99.6%; Score 1362; DB 4; Best Local Similarity 99.6%; Fred. No. 2.1e-150; Matches 259; Conservative 0; Mismatches 19;
                                                                                                                                                                                                                                                                                                       OWENTER REMODEL FORM

COMPUTER. IN FOR COMPACIDE

COMPUTER. IN FC COMPACIDE

COMPACINE STERE: COMPACIDE

SOFFATHER. (Generatech)
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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TITLE OF INVENTION: PURIFIED FORMS OF DNASE
UNWHERE OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MANE: JOHNETON, SEAR
REGISTRATION NUMBER: 35, 910
REPERRENCE/DOCKET NUMBER: P0747C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 660/25-3562
TELEPHONE: 860/25-3641
IRPOMATION POS REQ ID NO: 1;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/638,112
PILING DATE: 09-Aug-2000
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application PC/TUS9305136
GENERAL INFORMATION:
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APPLICATION NUMBER: 08/942561
FILLING DATE: 01-0CT-1997
ATTORNEY/AGENT INFORMATION:
                                                ADDRESSEE: Genentech, Inc.
                                                                           STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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TYPE: Amino Acid
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181 WSSIRLWTSPTFQWLIDDSADTTATFTHCAYDRIVVAGMLLRGAVVPDSALPFNEQAAYG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.3%; Score 1358; DB 4; Length 260; 99.2%; Pred. No. 4e-150; tive 1; Mismatches 1; Indels 1
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TELEX: 910/371-7168
INPORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 260 maino acids
TYPE: Amino Acid
                                     TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                  . 260 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.24
Matches 258; Conservative
                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Linear
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TELEFAX:
                                                                                                                                                                                                                                  LENGTH:
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99.3%; Score 1358; DB 4, Length 260;

Best Local Similarity 99.3%; Pred, No. 4e-150.

Best Conservative 1, Mismatches 1, Indels
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WEINTOW THER: 3.5 Linh, 1.44 Mb floppy disk MEDIOW THER: 3.5 Linh, 1.44 Mb floppy disk MEDIOW THER: 3.5 Linh, 1.44 Mb floppy disk COMPUTER: 1.8M FO COMPATIBLE DISK DOPERATION SYSTEM: 1.6-TONO-MEDION SYSTEM: 1.6-TONO-MEDION NOWER: 1.4-Dun-196

APPLICATION NOWER: 10/00/661,831

TELECOMMUTICATION NOWER: 15,910

TELECOMMUTICATION NOWER: 10/00/841

TELECOMMUTICATION NOWER: 10/
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TILTAN DATE: 14-Un-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
NAVE: "OBMISSOR, 50-0.
NAKE: "OBMISSOR, 50-0.
NAKE: "OBMISSOR, 50-0.
NEMERINATION NUMBER: 35,-00-0.
TREADEWNINGARIES, 52-36-36
TREADERN: 410/371-7164
INFORMATION FOR SED ID NO: 2: SECURIC CHRACKERISTICS: LENGTH: 260 amino acide TYPE: Amino Acide TYPE: Amino Acide Amino Am
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61 DTYHYVVSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120
                                                             61 DIYHYVVSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPALVRFFS 120
                                                                                                                                                                          121 RFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGCSYVRPSQ 180
                                                                                                                                                                                                                   181 WSSIRLWISPTFOWLIPDSADITATPIHCAYDRIVVAGWLLRGAVVPDSALPFNFQAAYG 240
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Sequence 4. Application US/08663831
Sequence 1. Application US/08663831
Septicon 1. Lararius, Robert A. Application 1. Lararius 1. Lararius 1. Lararius 1. Lararius 2. Lararius 1. Lararius 1. Lararius 2. Lararius 1. La
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99.3%; Score 1357; DB 4;
Best Local Similarity 99.2%; Pred. No. 5.2e-156;
Best Local Similarity 99.2%; Pred. No. 5.2e-156;
Miches 259; Conservative 0; Mismatches 2;
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MEDIUM TYER: 3.5 inch 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winheatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/663,831 FILING DATE: 14-Jun-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 LSDQLAQAISDHYPVEVMLK 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 LSDQLAQAISDHYPVEVMLK 260
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NAME: JOHNSON, SGAN A.
REGISTRATION NUMBER: 35,910
REFERENCE/DOCKET NUMBER: 91047
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 260 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELBFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: Amino Acid
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CLASSIFICATION:
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                                                                                               Gaps
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Score 1358; D8 4; Length 260;
Pred. No. 4e-150;
0; Mismatches 2; Indels
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Pred. No. 4e-150;
1; Mismatches 1; Indels
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APPLICANT: Lacarus, Robert A.
APPLICANT: Pan, Clark Qun
TITLE OF INVENTION: HIMAN DARS I HYPERACTIVE VARIANTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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Thorsessee: Genentech, Inc.
Thorses: Genentech, Inc.
CITY: South San Francisco
CITY: South San Francisco
COUNTRY: USA
ZIP: 94080
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; Sequence 15, Application US/08663831
; Patent No. 6391607
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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      Query Match
Best Local Similarity 99.2%;
Matches 258; Conservative
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TYPE: Amino Acid
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Matches 258, Conservative
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1 LKIAARNIQTEGSTKONSNATLVSYIVQIISRYDIALVQEVRDSHLTANGKLLDNLNQDAB 60
76 LKIAARNIQTEGSTKOSSNATLVSYIVQILSRYDIALVQEVRDSHLTANGKLLDNLNQDAB 135
61 DIYHYVVSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRPFS 120
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99.38; Score 1357; DB 1; Length 346;
Bett Local Similarity 99.28; Pred. No. 8.1e-150.
Matches 258; Conservative 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                             APPLICANT STREAM, SECTION J.
APPLICANT SHINKOWSHY S.
TITLE OF INVENTION: PURFIED FORMS OF DNase
CORRESPONDENCE ADDRESS:
ADDRESSES: Generace, Inc.
STREET: 460 Point Sea Remon Street
GTY: SOUTH SANGERS
                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08458367
Patent No. 5783433
GENERAL INFORMATION:
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TELEPHONE: 415/225-3562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: Amino Acid
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                                                                                                       RESULT 15
US-08-458-367-1
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99, 4001 90, 40

Sequence

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Sequence 59, P. Sequence 2, A. Sequence 2, A. Sequence 11, Sequence 11, Sequence 15, P. Sequence 15, P.

Sequence Sequence Sequence Sequence Sequence

sequence 5, M; sequence 6, M; sequence 6, M; sequence 112, p sequence 112, p sequence 112, p sequence 112, p sequence 113, p sequence 114, p sequence 115, p sequence 114, p sequence 5, M; sequence 5, M; sequence 3, M

US-10-005-675-15 US-09-825-012-5 US-10-133-065-3 US-10-133-065-2 US-10-133-065-2

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61 DTHYVVSEPLGRKSYKERYLFVYRPDQVSAVDSYXYDDGCEPCGNDTFNREPAIVRFFS 120
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100.0%; Score 1167; DB 14; Length 260;
Best Local Similarity 100.0%; Pred. No. 5e-145;
Matches 260; Conservative 0; Mismatches 0; Indels 0;
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| Publication On US2000173025A1
| GBNESAL INFORMATION | LOAD | LOAD |
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ORGANISM: Homo sapiens
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corre greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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Publication No. US2002012312A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
Baron, Will F.
TITLE OF INVENTION: HUMAN DNASE
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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181 WSSIRLWISPPROALISOSADTIATTHANDRIVAGGLAGAVVDDALPRRQAAV 240
181 WSSIRLWISPPROALISOSADTIATTHANDRINIVAGGLAGAVDDSALPRRQAAY 240
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Pred. No. 1.1e-144;
1; Mismatches 0; Indels 0
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Sequence 5, Spincardon 18/09825012
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September 141912-256800
FILE SEPRENCE: 411912-256800
FILE SEPRENCE: 411912-256800
FILE SEPRENCE: 2001-04-03
CURRENT PALIAND DATE: 2001-04-03
PRICE FLICATION NUMBER: 08 0008049.9
PRICE FLICATION NUMBER: 08 0008049.9
PRICE FLICATION NUMBER: 08 SEQ ID NOS: 102
SOFTMARE: Patentin Version 3.1
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Publication No. US20020173025A1
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Matches 259; Conservative
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ORGANISM: Homo sapiens
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       Length 260;
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99.6%; Score 1362; DB 10;
99.6%; Pred. No. 1.8e-144;
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CORRESPONDENCE ADDRESS:
ADDRESSE: Generacech, Inc.
STREET I DNA Nay
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STREET I DATE SOUTH SAN FRACISCO
STATE: CALIFORNIA
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DTYHYVVSEPLGRNSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120
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121 RFTEVRERIY TVELIARGORVAEIDALYDVILDVQEKWGLEDWLMGORNAGGSYRREG 180
181 RFTEVRERIY TVELIARGORVAEIDALYDVILDVQEKWGLEDWLMGORNAGGSYRREG 180
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    Length 260;
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                                                           Indels
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| Publication No. US2000173025A1
| GBNURAL INFORMATION No. US2000173025A1
| APPLICANT: Lacarus, Robert A. APPLICANT: Pan. Clark Qun
| ITTLE OF INVENTION HUNAN DAMAS I HYPERACTIVE VARIANTS
| TILE OF INVENTION HUNGERS: US/10/105.306
| CURRENT FALLYCATION MURSES: US/10/105.306
| CURRENT FALLYCATION WURSES: US/10/105.306
| CURRENT FALLYCATION WURSES: US/10/105.306
| RRIOR FALLNG DAFE: 2002-05.21
Score 1362; DB 14;
Pred. No. 1.8e-144;
0; Mismatches 1;
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Pred. No. 1.8e-144;
0; Mismatches 1;
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Query Match
Best Local Similarity 99.6%;
Matches 259; Conservative
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Best Local Similarity 99.6
Matches 259; Conservative
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ORGANISM: Homo sapiens
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181 WSSTRAMTSFTEQWI.TDSRDTTATFTHOADDRIVAGMILRGAVVDSSALPRIPGAN'G 240
181 WSSTRAMTSFTEQWI.TDSRADTTATFTHOADDRIVAGMILRGAVVDSSALPRIPGAN'G 240
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                                                                                       Gaps
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                      Ouery Match

99.6%; Score 1362; DB 14; Length 260;
Best Local Similarity 99.6%; Pred. No. 1.8e-14;
Matches 259; Conservative 0; Mismatches 1; Indels 0
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TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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Publicate to Application UN/A0074509
Publicate to Morphylogo and Mill P.
TYTHE OF INVESTOR: **ANTINE TO A SEQUENCE **ANTINE TO A SEQUENCE **ANTINE TO A SEQUENCE **ANTINE TO A SEQUENCE **ANTINE SEGUENCE A SEQUENCE **ANTINE SEGUENCE **ANTINE SE
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TYPE: Amino Acid
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SEQUENCE CHARACTERISTICS:
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ZIP: 94080
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US-10-074-509-4
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Sequence 14, Application US/10005306

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121 RFTEVREPALVDLHAARGDAVAELDALYDVILDYQEKWGLEDVALXGDFNAGCSYVRSG 180
121 RFTEVREFALVDLHAARGDAVAELDALYDVLDVQEKWGLEDVALXGDFNAGCSYVRSG 180
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Best Local Similarity 99.6%; Pred. No. 18e-144.

Matches 259; Conservative 0; Mismarches 1; Indels 0;
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                PEDICADET. COMPANY COMPOUNDED FOR TATGETING THILE REFERENCE 4.313-25609 CURRENT FALTICATION NUMBER: US 00/9.25,012 CURRENT FALTICATION NUMBER: US 00/1.37,159 PRIOR PAPLICATION NUMBER: US 00/237,159 PRIOR PLIANG DATE: 2001-04-02 PRIOR PLIANG DATE: 2000-04-03 PRIOR PLIANG DATE: 2000-04-03 PRIOR PLIANG DATE: 2000-04-03 WINDERS OF SEQ. 10 NOS: 1/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-005-675-14
APPLICATION NUMBER: 08/459909
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Patent No. US20020122798A1
GENERAL INFORMATION:
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121 RFTBVREFATVELHAAFODAVAIDALYOVIDVOEKWGLEDVMAKGDFNAGGSYVRBSQ 180
121 RFTBVREFATVELHAAFODAVAIDALYDVIDVOEKWGLEDVMAKGDFNAGGSYVRBSQ 180
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                                                            APPLICANT LARANDIA RODER A.
APPLICANT PARADIA RODER A.
APPLICANT PARADIA CLARK QUANTER
THIS BEREREKCE POLOCICIE
CURRANT APPLICATION NUMBER: US/10/005,306
CURRANT APPLICATION NUMBER: 08/663,931
PRIOR APPLICATION NUMBER: 08/663,931
PRIOR APPLICATION NUMBER: 1985-06-14
NUMBER OF SED ID NOS: 17
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MEDIUM TYPE: 3.5 inch, 1.44 MD floppy disk
COMPUTER: IRN FC compatible
OPREATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOTAL STATE OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOFTWARE: WinPatin (Genemicach)
CURRENT APPLICATION NOWER: 05/10/005,675
FLINED APPLICATION NOWER: 05/10/005,675
CLASSIFICATION: cUbrnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/669306
FILING DATE: 25-8ep-2001
APPLICATION NUMBER: 08/873506
FILING DATE: 08-Dec-1999
APPLICATION NUMBER: 08/643195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 LSDOLAOAISDHYPVEVWLK 260
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Publication No. US20020173025A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             ; SEQ ID NO 14
i LENGTH: 260
i TYPE: PRT
c ORGANISM: Homo sapiens
US-10-005-306-14
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DIYHYVVSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 WSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAYG 240
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                                                                                                                                                                                                                                                                                                                                                                                           73 LKIAAFNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAP
                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                           Length 341;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/348284
FILING DATE: 30-00. 082000077267A1-1994
APPLICATION NUMBER: 08/116186
FILING DATE: 02-569-1993
APPLICATION NUMBER: 07/89300
                                                                                                                                                                                                                 Query Match
99.6%; Score 1362; DB 15;
Best Local Similarity 99.6%; Pred. No. 2.7e-144;
Matches 259; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10155407A
Publication No. U32030775741
GREAL INFORMATION: John J.
STRICANT: Frenz. John J.
SILMONELL, Reven J.
SILMONELL, Reven J.
SILMONELL, Reven J.
SILMONELL, PROPERTION: PURIFED FORMS OF DAMAGE
NUMBER OF SEQUENCES: 18
CORRESPONDENCES 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA.
APPLICATION HUMBER: US/10/155,407A
FILING DATE: 22-484-2007
CLASSIFICATION: «UNKNOWN)
PRING APPLICATION HUMBER: 08 638112
FILING DATE: 11-Awg-2000
APPLICATION HUMBER: 08 648125
FILING DATE: 11-Awg-2000
APPLICATION HUMBER: 08/94261
FILING DATE: 01-OCT-199756
                                                                                              TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19-Apr-1996
APPLICATION NUMBER: 08/409631
FILING DATE: 22-Mar-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: Californía
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SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acids
TYPE: Amino Acid
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ZIP: 94080
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                                                                                                   1 LKIAAFNIQTFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAP
                                                                                                                                                                                                                                DTYHYVVSEPLGRKSYKERYLFVYRPDQVSAVDSYYYDDGCEPCGNDTFNREPAIVRFFS
                                       Gaps
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         99.6%; Pred. No. 2e-144; indels ive 0; Mismatches 1; Indels
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COMPUTE: TEALBALE FORM:
MEDINA TYPE: 3.5 INC. 1.44 Mb floppy disk
COMPUTE: INPER: 3.5 INC. 1.06 Mb least
SOFTWARE: WAITPEIN (Generace)
FILIND DATE: 10 CHESCOND 1.06 INC. 1.06 IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
TILLS OF UNIVERTION: Anti-Infective Therapy
NUMBER OF SEQUENCES, 25
CORRESPONDENCE ADDRESSES:
COUNTY:: GOLD San Francisco
COUNTY:: GOLD San Francisco
COUNTY:: GOLD San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Johnston, Sean A. REGISTRATION NUMBER: 35,910
REFERENCE/DOCKET NUMBER: P0530P1C10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 LSDQLAQAISDHYPVEVMLK 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/10005675
Publication No. US20030044403A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSDQLAQAISDHYPVEVMLK 260
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TELEFAX: 650/952-9881
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              Best Local Similarity 99.6
Matches 259; Conservative
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US-10-005-675-13
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61 DTYHYVVSEPLGRKSYKERYLFYYRPDQVSANDSYYYDDGCEPCGNDTFNREBALYRFS 120
318 DTYHYVVSEPLGRUSYKERYLFYYRPDQVSANDSYYDDGCEPCGNDTFNREBALVRFFS 377
318 DTYHYVVSEPLGRUSYKERYLFYYRPDQVSANDSYYYDDGCEPCGNDTFNREBALVRFFS 377
121 RFTEVREFALVPLHAAPCDAVAELDALYDVYLDVQEKWGLEDVMIMGDFNAGCSYVRPSQ 180
                                                                                               258 LKIAAFNIQIFGETKMSNATLVSYIVQILSRYDIALVQEVRDSHLTAVGKLLDNLNQDAP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            378 RFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWCLEDVMLWGDFNAGCSYVRPSQ 437
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418 WSSIRLWISPIRGWLIPDSADITAIPHAYDRIUWAGWLLRGAVVPDSALPRRGAN'G 97
418 WSSIRLWISPIRGWLIPDSADITAIPHAYDRIUWAGWLLRGAVVDSALPRRGAN'G 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 RFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGLEDVMLMGDFNAGGSYVRPSØ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Humanised HMFG1 Fd - DNase I fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARBEAL, INTERMATION:
APPLICAWY: YOUNG, Robert
TITLE OF UNEWRITON: Compound for Targeting
FILE REPRENCE: 4119.256600
FILE REPRENCE: 4119.256600
FILE PREPARENCE: 2001.40-03
CHRENT PALLAND DATE: 2001.40-03
PRIOR PELICATION NUMBER: US 60/237,159
PRIOR PELICATION NUMBER: GB 0008049.9
PRIOR PELICATION NUMBER: GB 0008049.9
PRIOR PELICATION NUMBER: GB 0008049.9
PRIOR SELING DATE: 3000-04-03
SOFTMARR: PARENTIN VERSION 3.3.
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Patent No. US20201279941
GENERAL INFORMATION:
APPLICANT: Young, Robert
TITLE OF INVENTION: Compounds for Targeting
FILE REPRENCE: 4319.1-256808
                                                                                                                                                                                                                                                             241 LSDQLAQAISDHYPVEVMLK 260
                                                                                                                                                                                                                                                                                   496 LSDQLAQAISDHYPVEVMLK 515
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 38, Application US/09825012 Patent No. US20020122798A1
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                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-09-825-012-38
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Query Match

Query Match

Query Carel Similarity 99:4%, Pred. No. 28-144, No. 28-144, No. 28-144, No. 28-144, No. 28-144, O. Mismatches 1, Indels 0, Matches 259, Conservative 0, Mismatches 1, Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 99.6%; Score 1362; DB 10; Length 515; DB et Local Similarity 99.6%; Pred. No. 498-144 Merches 259; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Humanised HMFG1 Fd - DNase I fusion
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                             NAME: Evans, David W. REGISTRATION NUMBER: NONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 LSDOLAGAISDHYPVEVMLK 260
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           ATTORNEY / AGENT INFORMATION:
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320 DYHYVVSBCANSYKERYLFVXPDQVSAVDSYYXDDGCEPCGNDTFNRRPAIVFFS 379 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION: Humanised HMFG1 Fd - DNase I fusion US-09-825-012-76
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CURRENT PILLING DATE: 2001.04.03
FRIOR PELICATION WHORER: 108 60/237,159
FRIOR PELICATION WHORER: 108 60/237,159
FRIOR PELILING DATE: 2000-04-03
FRIOR PELLING DATE: 2000-04-03
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ORGANISM: Artificial Sequence
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